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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

ACCESSION VERSION AK019655 LOCUS DEFINITION RESULT 1 AK019655

AK019655

MRNA linear HTC
Mus musculus adult male testis cDNA, RIKEN full-length
library, clone:4930486E09:ring finger protein 30, full sequence. AK019655 AK019655.1 GI:12859964 full insert HTC 19-JAN-2002

SOURCE KEYWORDS HTC; CAP trapper.

Mus musculus (strain:C57BL/6J) adult male testis cDNA to mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library clone:4930486E09.

ORGANISM Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

REFERENCE AUTHORS REFERENCE TITLE JOURNAL MEDLINE PUBMED Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253 10349636

MEDLINE PUBMED JOURNAL AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muzamatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)

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Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S.
Submitted (18-AUG-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                               cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
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/db_xref="MGD:MGI:1912089"
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|. .485
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                                                                                                                                                      1234 GAGGAGGGCAATGCGGGGGTGGAAGGAGGAGGGTGCCAGAAGGCTCAGGCCTG 1293
                                                                                                                                                                                                                                                         1174 ATCGACTTCCAGCCGGGCGCCGCTGGGGATGAAGAGGATGACGACATGGCTTTGGATGGG 1233
                                                 1294 CACTGACCCGACTCTGATCCAGAGCGCACACCCGAAGCGGAGCCAAGGGATGCTGAGGA 1353
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GAGGAGGGCAATGCGGGGCTGGAGGAGGAGCGGCTGGACGTGCCAGAAGGCTCAGGCCTG
                                                                                                                                                                                                        ATGGACTTCCAGCCGGGGCGCCGCCTGGGGGATGAAGAGGATGACGACATGGCTTTGGATGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: genome-res@rtc.riken.go.jp
Thermostabilization and thermoactivation of thermolabile enzymes by
Trehalose and its application for the synthesis of full length cDNA
(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                further details.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Chie Owa
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                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Mus musculus C57BL/6J heart"
/tissue_type="heart"
/note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia / with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T 3'); double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima
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/db_xref="taxon:10090"
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Pred. No. 9.9e-117;
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Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Inotani, K.,
Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T.,
Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T.,
Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K.,
Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T.,
Watahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.,
Watahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.,
RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BB732046 RIKEN full-length enriched, 12 days embryo whole body Mus musculus cDNA clone E970020A01 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000) wagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                          encyclopedia: real-time sequence clustering for construction of nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000) Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: genome-res@gsc.riken.go.jp/
URL:http://genome.gsc.riken.go.jp/
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                                                                                          /clone_lib="RIKEN full-length enriched, 12 days embryo
                                                                                                                            /db_xref="taxon:10090"
/clone="E970020A01"
                                                                                                                                                                                               /strain="C57BL/6J"
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/dev_stage="12 days embryo"
                              /tissue_type="whole body"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequencer. Genome Res.
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                                     AUTHORS
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High-efficiency full-length cDNA cloning
                                                                                                                                                                                                     HTC; CAP trapper.

Mus musculus (strain:C57BL/6J) adult male testis cDNA to mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                    AKO16235
957 bp mRNA linear HTC 19-JAN-Mus musculus adult male testis cDNA, RIKEN full-length enriched
                            Carninci, P. and Hayashizaki, Y.
                                                                                                                                                      Mus musculus
                                                                                       Mammalia; Eutheria;
                                                                                                                          Eukaryota;
                                                                                                                                                                                  clone:4930566102.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; This clone is among a rearrayed set of 15,247 clones from 11 embryo cDNA libraries (including preimplantation stage embryos from unfertilized egg to blastocyst, embryonic part of E7.5 embryos, extraembryonic part of E7.5 embryos, extraembryonic part of E7.5 embryos, extraembryonic part of E7.5 embryos ovary cDNA library. Average insert size 1.5 kb. All source libraries are cloned unidirectionally with Oligo(dr. clone) and control ovary cDNA libraries are cloned unidirectionally with Oligo(dr. clone)
                                                                                                             Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             under-representation on the X chromosome, Genet 7: 1967-1978."
119 c 151 q 62 t
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8S Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hiraoka, T., Hori, F., Hume, D., Imotani, K., Ishi, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Schrimi, L., Shibata, X., Shibata, Y., Shinagawa, A., Shiraki, T., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yamanaka, I., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and
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                Please visit our web site (http://genome.gsc.riken.go.jp/) for
                                                                                                                                   Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
                                                                            URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222
Fax:81-45-503-9216)
further details.
                                                                                                                                                                                                                                                                                                        Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
                                                                                                                                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                     Hayashizaki, Y
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                                                                               JOURNAL
                                                                                                                                                          TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 806 AGGACAACAGCCGCAGACAGAAGCAACTGTTAAACCAGAGGTTCGAGACCCTGTGCGCGG 865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   552
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGCAGCGCGTGCGGGGCCTCATCCGCCAGTACGGAGACCACTTGGAGG 973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTTTGGAGGAGCGCAAGGGCGAACTGCTTCAAGCACTGGCCCGGGAGCAGGAGGAGAAGT 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTTTGGAGGAGCGCAAGGGCGAACTGCTTCAAGCACTGGCCCGGGAGCAGGAGGAGGAAGT 925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGCAGCGCGTGCGGGGCCTCATCCGCCAGTACGGAGACCACTTGGAGG 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5 GAGAGAGAGAGAGACCCATTTTTTTTTTTTTTTTYN 3'], CDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI. Host: DH10B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ROT = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 418)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clone UUGC1M0349D21 F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AZ507637
                              Unpublished (2000)
Contact: Robert B. Weiss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1M0349D21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
                                                                                                                                                          Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AZ507637.1 GI:10688953
University of Utah Genome Center
                                                                                                                  plasmid inserts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
/strain="0578L/6J"
/db_xref="FANTOM_DB:4930566102"
/db_xref="MGD:MGI:1908652"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . 957
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 Mismatches

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FEATURES
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                                                                                                                                                                                                                                               DEFINITION
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                         REFERENCE
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     AUTHORS
                                                                                                ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1345 TGCTGAGGATCTGCGCAGAGACCACCGCGCCCACCAAGCTCGGCTTCCCGGCCCCCGGGAAG 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                               1405 GTTCTCAATAAAGGACTCAAGTGTCCC 1431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              352 TGCTGAGGATCTGCGCAGAGACCACCGCGCCACCAAGCTCGGCTTCCCGGCCCCCGGGAAG 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              292 GTTCTCAATAAAGGACTCAAGTGTCCC 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0349 row: D column: 21
Seg primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     University of Utah
Rm. 308, Biomedical
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Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Class: plasmid ends
                                                                                                                                                                                                                  BB140247 RIKEN full-length enriched, adult male bone Mus musculus CDNA clone 9830168H24 3', mRNA sequence.
                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 316)
                                                                                                  Mus musculus
                                                                                                                                                                                                  BB140247
                                                                                                                                                                                                                                                                        BB140247
Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci
                                                                                                                                                 EST
                                                                                                                                                                        BB140247.1 GI:8795184
                                                                                                                       house mouse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114)gblaFf129072.1), a copy-number inducible derivative of plasmid Rl. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab_host="E. Coli strain XI10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for amplicillin resistance."

107 c 137 g 88 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (http://www.jax.org/resources/documents/dnares/). The DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:10090"
/clone="UUGC1M0349D21"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10.3%; Score 147; DB 17; 100.0%; Pred. No. 3.1e-59; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           on/Qualitiers
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BASE COUNT
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                         1198 GGGGATGAAGAGGATGACCATGGCTTTGGATGGGGAGGAGGAGGCAATGCGGGGCTGGAG 1257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
                                                                                                                      Local Similarity
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci, P. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Carninci,P., Nishiyama,Y., Westöver,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Yomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
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Hitozane,T., Hori,F., Ishii,Y., Ishikawa,T., Ishikawa,T., Itoh,M.,
Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N.,
Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M.
Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.,
Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata,Y.,
Suzuki,H., Suzuki,H., Tagawa,A., Shiraki,T., Sogabbe,Y., Sugahara,Y.,
Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tominaga,N., Toya
T., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yamanaka,I.,
Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshino,
M., Muramatsu,M., and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Nishiyama,Y., Westover,A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       further details
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
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                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                  modified pBluescript KS(+) after bulk excision from Lambda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Site_1: Sal1; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken
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/dev_stage="adult"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: genome-reségsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci,P., Nishlyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
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Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)

Carninci,P. and Hayashizaki,Y.
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                             visit our web site (http://genome.rtc.riken.go.jp) for
                                          /dev_stage="adult"
/lab_host="DH10B"
             /note="Site_1:
                                                                                                                                     /sex="male"
                                                                                                                                                                                                    /db_xref="taxon:10090"
/clone="9830128L01"
                                                                                                        /tissue_type="bone"
                                                                                                                                                      /clone_lib="RIKEN full-length enriched, adult male bone"
                                                                                                                                                                                                                                                           organism="Mus musculus"
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SalI; Site_2: BamHI; cDNA library was
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                                                                                                                                          Email: genome-res@rtc.riken.go.jp
Thermostabilization and thermoactivation of thermolabile enzymes by
Thermostabilization and thermoactivation of thermolabile enzymes by
Trehalose and its application for the synthesis of full length cDNA
(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
                                                                                                                                                                                                                                                                               3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-9145
Fax: 81-298-36-9098
                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
Contact: Chie Owa
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                                                                                                                Please visit our web site (http://genome.rtc.riken.go.jp) for
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/strain="C57BL/6J"
                    /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1237 GAGGGCAATGCGGGG 1251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AW918753 378 bp mRNA linear EST 25-MAY-2000 EST350057 Rat gene index, normalized rat, norvegicus, Bento Soares Rattus norvegicus cDNA clone RGIEX57 5' end, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                   The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lee, N.H., Glodek, A., Chandra, I., Mason, T.M., Quackenbush, J., Kerlavage, A.R. and Adams, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AW918753.1 GI:8084538
                                                                                                                                                                                                                                                                                                              This clone is available through the ATCC, tel#703-365-2700 for further information \frac{1}{2}
                                                                                                                                                                                                                                                                                                                                                                                               Tel: (301)-838-3529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Lee,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus
                                                                                                                                                                                                                                                                                          Seq primer: M13 Reverse
                                                                                                                                                                                                                                                                                                                                                            Email: nhlee@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 378)
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                                                                                                                                                                                                                                                                                                                                                                              (301)-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Index
                        87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia
) with a modified polylinker; Site_1: Not I; Site_2: Eco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Mus musculus C57BL/6J heart"
/tissue_type="heart"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:10090"
/clone="1020006G17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
Xho1; Estimated insert size approx.1 kb"
a 100 c 122 g 69 t
                                                                                 /lab_host="SOLR"
                                                                                                         /tissue_type="mix - brain, ovary, placenta,
liver, embryo, heart, muscle, spleen"
                                                                                                                                                 Bento Soares"
                                                                                                                                                                 /clone_lib="Rat gene index, normalized rat, norvegicus,
                                                                                                                                                                                         /db_xref="taxon:10116"
/clone="RGIEX57"
                                                                                                                                                                                                                                /organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         118 GAGCTGAG 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          715 GAGCTGAG 722
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized AV canal at 16.5 dpc library cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seq primer: M13 Forward POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: msoares@blue.weeg.uiowa.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 456)
Bonaldo, M.F., Lenno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BE099923 456 bp mRNA linear EST 13-JUN-
UI-R-BJ1-atl-f-12-0-UI S1 UI-R-BJ1 Rattus norvegicus cDNA clone
UI-R-BJ1-atl-f-12-0-UI 3', mRNA sequence.
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          73 a
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                                                                                                                                                                               /clone_lib="UI-R-BJI"
/clone_lib="UI-R-BJI"
/clone_lib="UI-R-BJI"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_l: Not I; Site_2: Eco RI; The UI-R-BJI library is a subtracted library derived from the following tissues: atrium at 16.5 dpc, ventricle at 16.5 dpc, AV canal at 16.5 dpc, atrium at 15 dpc, ventricle at 15 dpc, AV canal at 15 dpc, ventricle at 13 dpc, and adult heart. For a detailed description of the library from which this
                                                                                                                    clone was derived, please visit our web site at ratest.eng.uiowa.edu. The subtraction has been previously described in (Bonaldo, Lennon and Soares, Genome Research
                           TAG_SEQ=GAACC"
                                                TAG_TISSUE=AV canal at 16.5 dpc
                                                                           6:791-806, 1996)
TAG_LIB=UI-R-BJ1
                                                                                                                                                                                                                                                                                                                                                                                                                                /strain="sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-BJI-atl-f-12-0-UI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Rattus norvegicus"
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114 g
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AI712700/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence contained an oligo-off track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-off track served to verify it as a clone from the normalized AV canal at 15 dpc library cDNA Library Preparation:

M.B. Soares Lab Clone distribution: clones will be available
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POLYA-Yes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         through Research Genetics (www.resgen.com)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seq primer: M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: msoares@blue.weeg.uiowa.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Program for Rat Gene Discovery and Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AI712700
UI-R-AF1-aau-e-02-0-UI-S1 UI-R-AF1 Rattus norvegicus
UI-R-AF1-aau-e-02-0-UI 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        University of Iowa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Soares, MB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genome Res. 6 (9), 791-806 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Normalization and subtraction: two approaches to facilitate gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                /lab_host="DHIOB (Life Technologies)"
/lab_host="PHIOB (Life Technologies)"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-AF1
library is a normalized library constructed from 15 dpc
rat atrioventricular (AV) canal. The tag is a string of 5
nucleotides present between the Not I site and the
oligo-dT track. The library was constructed as described
by Bonaldo, Lennon and Soares, Genome Research 6: 791-806
by Bonaldo, Lennon and Soares, Genome Research 6: 791-806
                 TAG_SEQ=GAAGG"
                                                                University of Iowa.
TAG_LIB=UI-R-AF1
                                   TAG_TISSUE=AV canal at 15 dpc
                                                                                                                                                                                                                                                                                                                                                       /clone="UI-R-AF1-aau-e-02-0-UI"
/clone_lib="UI-R-AF1"
                                                                                                                                                                                                                                                                                                                                                                                                     /strain="Sprague-Dawley
/db_xref="taxon:10116"
                                                                                              1996. Tissue provided by Jim Lin, Department of Biology,
                                                                                                                                                                                                                                                                                                                                     /dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Rattus norvegicus"
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BF284900/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   982 AAGCTGGTGGAGTCCGCCATCCAGTCCATGGAGGAGCCGCAGATGGCTCTCTCCACCTCCAG 1041
                                                                                                                         1042 CAGGC 1046
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                                                                                                                                                                                                                                                    Local Similarity
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EST449491 Rat Gene Index, normalized rat, Rattus norvegicus cDNA
Rattus norvegicus cDNA clone RGIEX57 3' sequence, mRNA sequence.
                                                                                                                                                                                                                                   65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Lee, NH
The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD
Tel: (301)-838-3529
Fax: (301)-838-9208
Email: nhlee@tigr.org
This clone is available through the ATCC,
tel#703-365-2700 for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2000)
Other_ESTs: EST350057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Malek,R.L., Cho,J., Lee,Y., Karamycheva,S., Parvizi,B., Pertea,G. Sultana,R., Tsai,J., White,J., Quackenbush,J. and Lee,N.H. Generation of ESTs from Normalized Rat Embryo, Bento Soares
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                                                                                                                                                                                                                                                                                                                                    /note="Vector: pT3T7Pac; Site_1: EcoR1; Site_2: Not1; Combination of ROV, RBR, RKI, RLI, RPL, RLU, REM, RMU, RHE, RPC, RPN"
                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Rat Gene Index, normalized rat, Rattus
norvegicus cDNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Rattus norvegicus"
/db_xref="taxon:10116"
/clone="RGIEX57"
                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="mixed tissue"
/lab_host="DH5-alpha"
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100.0%; Pred. No.
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                                                                                                                                                                                                                                     0; Mismatches
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     linear
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     EST 30-APR-1998
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    {\tt EST189742} Normalized rat heart, Bento Soares Rattus sp. cDNA clone RHEAM89 3' end, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The Institute for Genomic Research 9712, Medical Center Drive, Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Lee,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lee, N.H., Glodek, A., Chandra, I., Mason, T.M., Quackenbush, J.,
                                                                  Unpublished (1999)
Other_GSSs: RPCI-24-117M3.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 449)
                                                                                                                                                                                                                                                                                                                                          DNA sequence. AZ731346
                                                                                                                                                                                                                                                                                                                                                                            AZ731346 449 bp DNF RPCI-24-117M3.TV RPCI-24 Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seq primer: M13-21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fax: (301)-838-0208
Email: nhlee@tigr.org
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                         Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregeorgis,E., Russell,D., de Jong,P. and Fraser,C.M.
Mouse BAC End Sequences from Library RPCI-24
                                                                                                                                                                                                                                                                    Mus musculus
                                                                                                                                                                                                                                                                                                                           AZ731346.1 GI:12493317
                                                                                                                                                                                              Zhao,S., Nierman,W., Malek,J., Shatsman,S., Akinret,B., Levins,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                       house mouse.
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/note="Organ: heart; Vector: pT7T3Pac; Site_1: E
Site_2: NotI"
a 221 c 165 g 147 t
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/db_xref="ATCC (inhest):2007238"
/db_xref="taxon:10118"
/clone="RHEAM89"
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1, .638
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100.0%; Pred. No. 7.1e-20;
                                                                                                                                                                                                                                                                                                                                                                                                    DNA
                                       MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                               genomic clone RPCI-24-117M3,
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COMMENT
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RS Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Carninci,P., Endo,T., Fikuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,F., Ishii,Y., Ishikawa,T., Itch,M., Ishiyawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N., Kojima,Y., Koya,S., Kusakabe,M., C., Kawai,J., Kikuchi,N., Kojima,Y., Koya,S., Kusakabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y., Owa,C., Ozawa,Y., Saito,H., Sano,M., Sato,K., Shibata,K., Shibata,Y., Shigemoto,Y., Shitaki,T., Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Takahashi,F., Tateno,M., Tominaga,N., Tsunoda,Y., Watanabe,S., Yamamura,T., Yasunishi,A., Yokota,T., Yoshino,M., Muramatsu,M. and Hayashizaki,Y., Voshiki,A., Yoshino,M., Get al. 1999)

N.L. Unpublished (1999)

N.L. Unpublished (1999)
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                                                        URL:http://genome.gsc.riken.go.jp/
Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki
                                                                                                                                                                                                                                 Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-Cho, Tsurumi-ku, Yokohama, Kanagawa 230-
                                                                                                                                                    Email: genome-res@gsc.riken.go.jp,
                                                                                                                                                                                                                                                                                                                  Laboratory for Genome Exploration Research Group, RIKEN Genomic
                                                                                                                                                                                                                                                                                                                                                           Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AV361069 RIKEN full-length enriched, adult male eyeball Mus musculus cDNA clone 7530421L22 3', mRNA sequence.

AV361069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
Transcriptional sequencing: A method for DNA sequencing using RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       house mouse
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Clones are derived from the mouse BAC library RPCI-24. For BAC
Clones are derived from the mouse BAC library availability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC opage: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 117 row: M column: 3
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81-45-503-9216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /Cell_type="Spleen/Brain"
/Cell_type="Spleen/Brain"
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
/RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
library was cloned in the pTARBAC1 cloning vector at the
BamH1 sites using MboI partially digested male C57BL/6J
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/clone="RPCI-24-117M3"
/clone_lib="RPCI-24"
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Pred. No.
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                            RESULT 16
BG375657/c
                                                                                                                                                                                                                                           KEYWORDS
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                      MEDLINE
                                             JOURNAL
                                                                                  TITLE
                                                                                                       AUTHORS
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                                                                                                                                                                                                                                                                                        BG375657

440 bp mRNA linear EST 12-MAR-:
UI-R-CS0-btd-h-03-0-UI.s1 UI-R-CS0 Rattus norvegicus cDNA clone
UI-R-CS0-btd-h-03-0-UI 3', mRNA sequence.
Contact: Soares, MB
                        97044477
                                     Genome Res. 6 (9), 791-806 (1996)
                                                             discovery
                                                                        Normalization and subtraction: two approaches to facilitate gene
                                                                                              Bonaldo, M.F., Lennon, G. and Soares, M.B.
                                                                                                                                                  Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                  Rattus norvegicus
                                                                                                                                                                                                                    Norway rat
                                                                                                                                                                                                                                                         BG375657.1 GI:13300129
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                                                                                                                                            Rattus
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                                                                                                                   (bases 1 to 440)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BamHI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Site_1: Sal1; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  contributed to prepare mouse tissues. 1st strand cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="RIKEN full-length enriched, adult male eyeball"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="eyeball"
/dev_stage="adult"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:10090"
/clone="7530421L22"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.6%; Score 52;
100.0%; Pred. No.
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AUTHORS
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                                                                                    COMMENT
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Best Local
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                                                                                                                MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    999 CATCCAGTCCATGGAGGAGCCGCAGATGGCTCTCTACCTCCAGCAGGC 1046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: msoares@blue.weeg.uiowa.edu
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. The sequence tag present in the cDNA between the NotI site
and the oligo-dT track served to verify it as a clone from the
normalized rat heart pool library cDNA Library Preparation: M.B.
Soares Lab Clone distribution: clones will be available through
Research Genetics (www.resgen.com)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Program for Rat Gene Discovery and Mapping University of Iowa 451 Eckstein Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 8250 Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BG379943 441 bp mRNA linear IUI-R-CSO-bto-b-01-0-UI.S1 UI-R-CSO Rattus norvegicus UI-R-CSO-bto-b-01-0-UI 3', mRNA sequence.
University of Iowa
451 Eckstein Medical Research Building Iowa City,
                                                     Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
                                                                                                                                      Genome Res. 6 (9), 791-806 (1996)
                                                                                                                                                                     discovery
                                                                                                                                                                                                                        Bonaldo, M.F.,
                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus
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                                                                                                                                                                                                                                                                          Rattus
                                                                                                                                                                                                                                                                                                                                                                                  Norway rat.
                                                                                                                                                                                            Normalization and subtraction: two
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                                                                                                                                                                                                                                              (bases 1 to 441)
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/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-CS0
library is a normalized library constructed from the
following rat heart tissues: embryonic day 17, embryonic
day 19, embryonic day 21, adult day 1, adult day 12, adult
day 75, adult day 200. For a detailed description of the
library from which this clone was derived, please visit
our web site at ratest.eng.uiowa.edu. The subtraction has
been previously described in (Bonaldo, Lennon and Soares,
genome Research 6:791-806, 1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAG_TISSUE=rat heart pool TAG_SEQ=ATAAGATAAC"
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/clone_lib="UI-R-CS0"
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/db_xref="taxon:10116"
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                                                                                                                                                                                                                     Lennon, G. and Soares, M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3.4%; Score 48;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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8.7e-12;
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                                                                                                                                                                                            facilitate gene
     IA 52242,
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AV268013
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1048 AAGGAGCTGATCAACAAGGTCGGGGCAATGTCGAAGGTGGAGCTGGC 1094
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 250)

1 (bases 1 to 250)

RS Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishii, Y., Ishikawa, T., Icoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kojima, Y., Koya, S., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Owa, C., Ozawa, Y., Saito, H., Sano, M., Sato, K., Shibata, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Takahashi, F., Tateno, M., Tominaga, N., Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yasunishi, A., Yokota, T., Watahiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y. Contact: Yoshihide Hayashizaki
Laborattory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AV268013 RIKEN full-length enriched, adult male testis (DH10B) Mus musculus cDNA clone 4930532G16 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               house mouse.
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/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-CS0 library is a normalized library constructed from the following rat heart tissues: embryonic day 17, embryonic day 19, embryonic day 21, adult day 1, adult day 12, adult day 75, adult day 200. For a detailed description of the library from which this clone was derived, please visit our web site at ratest.eng.ulowa.edu. The subtraction has been previously described in (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)
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/strain="Sprague-Dawley"
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Pred. No. 2.6e-11;
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                                                                                                                                                                                                                              ACCESSION
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Best Local :
                                                                                                                            ORGANISM
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                                                                                                                                                                                                                                                BE095943

UI-R-BU0-apd-e-03-0-UI.sl UI-R-BU0 Rattus norvegicus UI-R-BU0-apd-e-03-0-UI 3', mRNA sequence:
1 (bases 1 to 386)
Bonaldo, M.F., Lenno
                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                       Rattus norvegicus
                                                                                                                                                                                                                              BE095943
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URL:http://genome.gsc.riken.go.jp/
Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T.,
Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and
                                                      Rattus.
                                                                                                                                                      Norway rat.
                                                                                                                                                                                                    BE095943.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and Hayashizaki,Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGASATTCRCGAGTTAATTAAATTAATCCCCCCCCCCCC 3']. CDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: Sall; 3' end: BamHI." a 66 c 75 g 44 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="4930532G16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by
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/dev_stage="adult"
/lab_host="DH10B"
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100.0%; Pr
Lennon, G.
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Pred. No.
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Hayashizaki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Locus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
MEDLINE
                                   TITLE
                                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1096 GGACGGCCGGAGCCAGGCTATGAGAGCATGGAGCAATTCTCTGTGA 1141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           346 GGACGGCCGGAGCCAGGCTATGAGAGCATGGAGCAATTCTCTGTGA 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: msoareséblue.weeg.uiowa.edu
The sequence contained an oligo-dT track that was present in the oligonuclectide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized ganglia library cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com)
                                                   Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertaa, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46;
                                                                                                                                                                                                                                                                                                 Bos taurus
                                                                                                                                                                                                                                                                                                                                                     EST
                                                                                                                                                                                                                                                                                                                                                                                                   500054 MARC 2BOV Bos taurus cDNA 5', BM087315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle
                                                                                                                                                                                                                  Bovidae; Bovinae;
                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                              BM087315.1 GI:16997943
                                                                                                                                                                                                                                                                                                                                                                                                                                                          BM087315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              451 Eckstein Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 8250 Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genome Res. 6 (9), 791-806 (1996) 97044477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POLYA=Yes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                    (bases 1 to 467)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.2%;
ilarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /lab_host="DH10B (Life Technologies)"
//lab_host="DH10B (Life Technologies)"
//lab_host="DH10B (Life Technologies)"
//lab_host="DH10B (Life Technologies)"
//lab_host="DH10B (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-BU0
library is a subtracted library derived from a mixture of
eye and ganglia tissues. For a detailed description of the
library from which this clone was derived, please visit
our web site at ratest-eng ulowas derived, please visit
our web site at ratest-eng ulowa-edu. The subtraction has
been previously described in (Bonaldo, Lennon and Soares,
Genome Research 6:791-806, 1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TAG_TISSUE=ganglia
TAG_SEQ=GCAGAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TAG_LIB=UI-R-BUO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="Sprague-Dawley"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . 386
                                                                                                                                                                                                            Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 46;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                          467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 10; 1, 7.5e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4
                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 386;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                          EST 19-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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JOURNAL
MEDLINE
COMMENT
Search completed: December Job time: 2081 secs
                                                                                           B
                                                                                                                                                                                                                                                                        BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                      Query Match 3.2%; Score 46; DB 13; Length 467; Best Local Similarity 100.0%; Pred. No. 8.1e-11; Matches 46; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     source
                                                                               Genome Res. 11 (4), 626-630 (2001)
21180013
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BACKWARD: GTTTTCCCAGTCACGACG
Plate: 137 row: H column: 12
Seq primer: ATTTAGGTGACACTATAG.
Location/Qualifiers
1. .467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and -minmatch 12 options. PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                                                                                                                                           113 a
                                                                                                                                                                                                                                                                                                                                                                                                /organism="Bos taurus"
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/lab_bost="DH10B"
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                     3, 2002, 12:05:11
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EST189742 Normalized rat heart, Bento Soares Rattus sp. cDNA clone
DEFINITION
         RHEAM89 3' end, mRNA sequence.
         AA800245
ACCESSION
         AA800245.1 GI:2863200
VERSION
         EST.
KEYWORDS
         Rattus sp.
SOURCE
 ORGANISM
         Rattus sp.
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
         Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
REFERENCE
            (bases 1 to 638)
         Lee, N.H., Glodek, A., Chandra, I., Mason, T.M., Quackenbush, J.,
 AUTHORS
         Kerlavage, A.R. and Adams, M.D.
         Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
 TITLE
         Gene Index
         Unpublished (1998)
 JOURNAL
         Contact: Lee, NH
COMMENT
         The Institute for Genomic Research
         9712, Medical Center Drive, Rockville, MD 20850, USA
         Tel: (301)-838-3529
         Fax: (301)-838-0208
         Email: nhlee@tigr.org
         Seq primer: M13-21.
                Location/Qualifiers
FEATURES
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                /organism="Rattus sp."
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                                          Length 638;
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 Best Local Similarity
 Matches 595; Conservative
                         0; Mismatches
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                                           Indels
                                                  11;
                                                     Gaps
Qу
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    638 GGAGGAGGTGTGCCAGACCATTGAGGACAACAGCGGCAGAACAACAGCTGTTAAACCA 579
    843 GAGGTTCGAGACCCTGTGCGCGGTTTTGGAGGAGCGCAAGGGCGAACTGCTTCAAGCACT 902
Oy
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    578 GAAGTTCGAGACCCTGTGCGCGGTTTTGGAGGAGCGCAAGGGCGAGTTGCTTCAAGCGCT 519
    903 GGCCGGGAGCAGGAGAAGTTGCAGCGCGTGCGGGGCCTCATCCGCCAGTACGGAGA 962
Qу
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Qу
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Db
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638 bp

mRNA

AA800245

LOCUS

EST

linear

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AA800245
LOCUS
         EST189742 Normalized rat heart, Bento Soares Rattus sp. CDNA clone
DEFINITION
          RHEAM89 3' end, mRNA sequence.
          AA800245
ACCESSION
          AA800245.1 GI:2863200
VERSION
          EST.
KEYWORDS
SOURCE
          Rattus sp.
 ORGANISM
          Rattus sp.
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
REFERENCE
             (bases 1 to 638)
          Lee, N.H., Glodek, A., Chandra, I., Mason, T.M., Quackenbush, J.,
  AUTHORS
          Kerlavage, A.R. and Adams, M.D.
          Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
  TITLE
          Gene Index
          Unpublished (1998)
  JOURNAL
          Contact: Lee, NH
COMMENT
          The Institute for Genomic Research
          9712, Medical Center Drive, Rockville, MD 20850, USA
          Tel: (301)-838-3529
          Fax: (301)-838-0208
          Email: nhlee@tigr.org
          Seq primer: M13-21.
                  Location/Qualifiers
FEATURES
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                  /clone_lib="Normalized rat heart, Bento Soares"
                  /note="Organ: heart; Vector: pT7T3Pac; Site_1: EcoRI;
                  Site_2: NotI"
                             165 g
                                    147 t
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                     221 c
BASE COUNT
ORIGIN
Alignment Scores:
                                 Length:
                                              638
                    5.93e-75
Pred. No.:
                    778.00
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Score:
                                              4
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Percent Similarity:
Best Local Similarity:
                    91.81%
                                 Mismatches:
                                              8
                                              2
                                 Indels:
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Query Match:
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DB:
US-09-908-988B-2 (1-366) x AA800245 (1-638)
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Qy
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Db
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Db
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Qу
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Db
     336 GluGluAspAspAspMetAlaLeuAspGlyGluGluGlyAsnAlaGlyLeuGluGluGlu 355
Qy
         217 GAAGAGGATGACGAGGTGACTTTGGACGGGGAAGAGGGCAACACAGGGCTGGAGGAGGAG 158
Db
     356 ArgLeuAspValProGluGlySerGlyLeuHis 366
Qy
         157 CGGCTGGACGGCCAGAA-----GGTTTGCAC 131
Db
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638 bp

mRNA

linear

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OM protein - nucleic search, using frame_plus_p2n model
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MODEL-frame+_p2n.model -DEV=xlh

MODEL-frame+_p2n.model -DEV=xlh

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-DB=EST -QFMT-fastap -SUFFIX-rist -MINMATCH=0.1 -LOOPECL=0 -LOOPEXT=0

-UNITS-Dits -START-1 -END=-1 -MATRIX-blosum62 -TRANS-human40.cdi -LIST-45

-DCCALIGN=20 -MCDE-CCAL

-DCCALIGN=20 -MCDE-CCAL

-OUTFMT-pto -NORM-ext -HEAPSIZE-500 -MINLEN-2000000000

-USET -US09908988_eCCN_1_1_763_erunat_26112002_112155_11286 -NCPU-6 -ICPU-3

USER-US09908988_eCCN_1_1_763_erunat_26112002_112155_11286 -DEV_TIMEOUT=120

-NARN_TIMEOUT=30 -THREADS=1 -KGAPOP=10 -KARDEXT=0.5 -FGAPOP=6 -FGAPEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Minimum DB seg length: 0
Maximum DB seg length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YGAPOP-10 -YGAPEXT-0.5 -DELOP-6 -DELEXT-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-908-988B-2
1912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MNFTVGFKPLLGDAHNMDNL.....EGNAGLEEERLDVPEGSGLH 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               December 3, 2002, 13:08:10 ; Search time 2056 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16154066 segs, 8097743376 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                          gb_est1:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     em_esthum: *
                                                                                                                                                                                                                                                                                                                                                                                                                                             em_htc:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         em_estro:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     em_estov:*
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                                                                                                                 em_gss_pln:*
em_gss_vrt:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

O	n	o o	0 0 1 8	Result
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44642 vw79b06 44642 vw79b06 019655 Mus mu 894237 601437 899066 fy64eC 42216 AJ44221 12700 UI-R-AF 12700 UI-R-AF 77673 fc50c07 7724411 bx04e1 58735 fc96b12	AL128 9800 Tectracoon BIII14696 602861723 BIII14696 60286172360 BG072860 BJ072360 BG6728823 602620959 BJ070440 BJ070440 BM726538 UT-E-EJU-BF205857 601868260 BJ074770 BJ074770 BF305857 601868260 BJ074770 BJ074770 BF305857 601891901 AW483766 56372 MAR BB662321 BB662321 AW918753 EST350057 AA443443 zw94605.r BG765856 602739688 BI891864 ZF637-3-0 AL1213681 Tectracdon BJ500196 BJ500196 AL736446 Danio rer BG769996 602745109	1754358 603 67761218 602 B520266 BGE B520266 BGE J033623 BJG 668403 AL66 668403 AL66 668403 AL66 J059953 BJG J059953 BJG J7284900 EST F284900 EST	iption 1661 BJ07 5618 RC0- 8535 6030 0114 4886 5619 RC0- 4060 6027	

ALIGNMENTS

REFERENCE AUTHORS	ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	LOCUS	BJ071661	RESULT 1
Xenopodinae; Xenopus. 1 (bases 1 to 595) Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and Kohara	xenopus laevis Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;	African clawed irog.	EST.	BJ071661.1 GI:17501850	BJ071661	laevis cDNA clone XL095b10 5', mRNA sequence.	BJ071661 NIBB Mochii normalized xenopus talloud library Aemopus	BJ071661 595 DP MKNA LITTER COLUMN CO		

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                                                                                CysGluValProThrCysSerLeuCysLysValPheGlyAlaHisLysAspCysGluVal 160
GCCCCTCTTTCCAGCATCTACAAAAGGCAGAAGAGTGAGCTGAGTGACGGCATTGCCATG
                  AlaProLeuProThrIleTyrLysArgGlnLysSerGluLeuSerAspGlyIleAlaMet 180
                                                             TGCGAGGTCCCTACCTGCTCCATGTGCAAAGTCTTTGGGGGCCCACAAGGACTGTGAGGTG
                                                                                                                                                                                                                                                       GAGCAGCACCTCATGTGTGAAGAGCACGAGGATGAGAAGATTAACATCTACTGCCTGAGC
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Unpublished (2001)
Contact: Tadasu Shin-i
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National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="vector: pBSRN3; Site_1: NotI; Site_2: EcoRI; cDNAs were oligo-dT primed and directionally cloned. Staging according to Nieuwkoop and Faber. Library is subtracted and was constructed by N. Garrett and A.M. Zorn, (Wellcome/CRC Institute). "
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/dev_stage="stage 25"
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/db_xref="taxon:8355"
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CysArgLysCysAlaAsnAspValPheGlnAlaSerAsnProLeuTrpGlnSerArgGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RCO&t2=RCO-FN0204-
161100-031-d06&t3=2000-11-16&t4=1)
Seq primer: puc 18 forward
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: +55-11-2704922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-Sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Simpson A.J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fax: +55-11-2707001
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1 (bases 1 to 555)
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                                                                                                                                                                                                                                                                                                                                                                         Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Organ: prostate_normal; Vector: pucl8; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="FN0204"
/dev_stage="Adult"
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Tissue Procurement: Life Technologies,
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Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T., Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,G.E., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G., Pertea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and Keele,J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FORWARD: AGGAAACAGCTATGACCAT
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Bovidae; Bovinae; B
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/tissue_type="pooled"
/lab_host="DH10B"
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/db_xref="taxon:9913"
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RCO&t2=RCO-FNO204-
161100-031-e06&t3=2000-11-16&t4=1)
Seq.primer: puc 18 forward
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 and
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                                                               /note="Organ: prostate_normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                      /clone_lib="FN0204"
/dev_stage="Adult"
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/db_xref="taxon:9606"
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Percent Similarity:

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                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                                                                                                                                                                 NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 868)
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                                                            found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLCM1722 row: j column: 18
                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                         BG764060.1 GI:14074713
                                                                                                        cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can
                                                    quality sequence stop: 863.
/organism="Homo sapiens'
/db_xref="taxon:9606"
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/clone="IMAGE:4862321"
/clone_1lb="NIH_MGC.49"
/clone_1lb="NIH_MGC.49"
/tissue_type="melanotic melanoma, high MDR (cell line)"
/lab_host="DH10B (phage-resistant)", Site_1: XhoI; Site_2:
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2: Note: this is a NIH_MCC
/note="Organ: skin; Vector: poTB7; Site_1: XhoI; Site_2: Note: this is a NIH_MCC
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                                                                             GGTAAAGGAAGAGCTGAGCCAGACAGTTTGACACGTTAGTATGCCATCCTGGATGAGAAG
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Tissue Procurement: Life Technologies,
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6030226906F1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5197560 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH-MGC http://mgc.nci.nih.gov/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
cLione distribution: MGC clone distribution information can be
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gGlnLysGlnLeuLeuAsnGlnArgPheGluThrLeuCysAlaValLeuGluGluArg
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                                                                                                                                                                                                                                                                                                                                                                          found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
http://image.llnl.gov
Plate: LLCM1712 row: p column: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1105)
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BG761218
                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can
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                                                                                                                                                                                                                                                                                                                                                           quality sequence stop:
/tissue_type="melanotic melanoma, high MDR (cell line)"
/lab_host="DHIOB (phage resistant)"
/note="organ: skin; Vector: poTBT, Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5 adaptor:
GECACGAK(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley)
                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4858622"
/clone_lib="NIH_MGC_49"
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                                                                                                                                                                                                             228 LysGlyGluLeuLeuGlnAlaLeuAlaArgGluGlnGluGlu-LysLeuGlnArgValAr ::: ||||||||:::||| ||||
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                                                                                                                                                                                                                                                                                                                                                                                                                                    sargGlnLysSerGluLeuSerAsp-GlyIleAlaMetLeuValAlaGlyAsnAspArgV 188
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                                                                                                                  AGGCCTCATCCAAGCAGTAACCCAGGAGGCAGTGGGACAAAGTCAACAAGCTGGTGGAAA
                                                                                                                                                    gGlyLeuIleArgGlnTyrGlyAspHisLeuGluGly---Ser-SerLysLeuValGluS 266
                                                                                                                                                                                         CAACTGGAGTTGGTGCAGGGATCAACGCAGGAGCAGGACGAAAAAGGTTAGCTACATCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                     GGGACAAAAGACTGAACTGAATAACTGGTATCTCCATGCTGGTGGCGGGGAATGACCGTG 669
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                                                                             erAlaIleGln-SerMetGluGluProGlnMetAlaLeuTyrLeuGlnGlnAlaLysGlu 285
                                         CTGCCATCCAAGTCCCTGGGAGAGCCGGGGGAAGCACCTACTCTTGATCGGCAGAGCACA 969
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RESULT 9
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jap
Tel: 81-45-503-9222
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Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A.
Arakawa, T., Carninci, P., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda
, Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Nomura, K., Ohno, M.,
, Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M.,
Okazaki, Y., Okido, T., Salto, R., Sakai, C., Sakai, K., Sano, H., Sasaki
, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H.,
, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H.,
Tagami, M., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T.,
Muramatsu, M., and Hayashizaki, Y.,
Muramatsu, M., and Hayashizaki, Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: genome res@gsc.riken.go.jp,

URL:http://genome.gsc.riken.go.jp,

Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh

Carninci,P., Shibata,Y., Muramatsu,M. and Hayashizaki,Y.

M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new

genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,

watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura

S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
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On Jul 28, 2000 this sequence version replaced gi:9571724.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fax: 81-45-503-92
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                                                                                                                                                                                                                                                                                                                                       prepare mouse tissues.
                                                                                                                                                                                                                                                                                                                                                                          CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Rike Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human Genome Sequences Mamm.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                further details.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Computational Analysis of Full-Length Mouse cDNAs Compared with luman Genome Sequences Mamm. Genome. 12, 673-677 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Computer-based methods for the mouse full-length cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Please visit our web site (http://genome.gsc.riken.go.jp/) for
/tissue_type="heart"
/dev_stage="16 days neonate"
                                                                                                                                                     /clone="D830041C10"
                                                                                                              'clone_lib="RIKEN full-length enriched, 16 days neonate
                                                                                                                                                                                 /db_xref="taxon:10090"
                                                                                                                                                                                                                        /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                   location/Qualifiers
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DEFINITION
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                                                                                                                                                         GluLeuSerAspGlyIleAlaMetLeuValAlaGlyAsnAspArgValGlnAlaValIle
                                                                                                                                                                                                                                                                  CGCATCAACATCTATTGTCTGAACTGTGAAGTGCCCACCTGTTCCTTGTGCAAGGTTTTT
                                                                                                            ThrGlnMetGluGluValCys 199
                                                                                                                                                                                                   GGCGCCCATAAGGACTGCCAGGTGGCTCCCCTGACTCATGTTTTCCAGAGGCAGAAGTCA
                                                                                  AGCCAGCTGGAGGACACCTGT
                                                                                                                                                                                                                                                                                                                                                           SerArgProLeuHisAlaLysAlaGluGlnHisLeuMetCysGluGluHisGluAspGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AspValPheGlnAlaSerAsnProLeuTrpGlnSerArgGlySerThrThrValSerSer 72
                                                                                                                                                                                                                                                                                                                               ACCAGGCCA---GAAAAAAATTGGACCAGCCC---ATGTGTGAAGAGCATGAAGAGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTCACGAAGCCTGTGGTCATTCTCCCTTGCCAGCACAACCTGTGCAGGAAATGTGCCAGT
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вJ033623
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   615 bp
NIBB Mochii normalized
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note-"Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
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121 GluGlnHisLeuMetCysGluGluHisGluAspGluLysIleAsnIleTyrCysLeuSer 140
                                No.:
                                                                                                    281 TGTAGACATGAAGTGGTGTTGGACAGACATGGCGTATATGGACTACAAAGGAACTTACTG
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                                                                                                                                                                                                                                                                                                                                                                                                      1 MetAsnPheThrValGlyPheLysProLeuClyAspAlaHisAsnMetAspAsnLeu
                                                     ValGluAsnIleIleAspIleTyrLysGlnGluSerSerArgProLeuHisAlaLysAla 120
                                                                                                                      CysArgHisGluValValLeuAspArgHisGlyValTyrGlyLeuGlnArgAsnLeuLeu
                                                                                                                                                                      TATTTGCCAACACGAGGAGGAAACACAGTAGCATCGGGTGGACGTTTTCGCTGCCCATCG
                                                                                                                                                                                          LeuTrpGlnSerArgGlySerThrThrValSerSerGlyGlyArgPheArgCysProSer
                                                                                                                                                                                                                                       CCCTGCCAGCATAATCTGTGTAGGAAGTGTGCGAGTGATATATTCCAGGCTTCCAATACG
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Tel: 81-559-81-6856
Fax: 81-559-81-6855
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Expressed genes in X. laevis embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kitayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-i, T. and Kohara
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Xenopodinae; Xenopus.
1 (bases 1 to 615)
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African clawed frog.
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BJ033623
BJ033623.1 GI:17414076
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type-""
/dev_stage="stage 15"
/dev_stage="stage 15"
/note="Vector: pBSRN3; Site_1: NotI; Site_2: EcoRI; cDNAs
were oligo-dT primed and directionally cloned. Staging
according to Nieuwkoop and Faber. Library is subtracted
and was constructed by N. Garrett and A.M. Zorn,
(Wellcome/CRC Institute)."
119 c 138 g 161 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="XL022f14"
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RESULT 11
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                                                                                                                                                                           10 LeuLeuGlyAspAla-----HisAsnMetAspAsnLeuGluLysGlnLeuIleCysPro
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                 ArgLysCysAlaAsnAspValPheGlnAlaSerAsnProLeuTrpGlnSerArgGlySer 67
                                                                                                                                          TTGATGGGNGGGGCGGCTGGGCCGAATCCCGAAGAAATTGAACGGCTTCTGATGTGTCCA 119
 AGGAAATGCGCCAACGATGTGTTT----
                                                                        ATATGTCTTGAAATCTACACCAAGCCCGTTGTTATTCTCCCCTGCCAGCATAACTTGTGC
                                                                                                    IleCysLeuGluMetPheSerLysProValValIleLeuProCysGlnHisAsnLeuCys 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr Web : www.genoscope.cns.fr
IMPORTANT: this sequence may contain errors. The Ciona intestinalis
library from which the clone was isolated may be contaminated with
cDNAs from bacteria or other Eukarya.
Directional larval cDNA library originate from Dr.M.Branno,
Stazione A.Dohrn, Naples, Italy, and was prepared in
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1 (bases 1 to 815)
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                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="directional larval cDNA library"
/note="Vector: pBluescript2SK+"
/ 146 c 194 g 213 t 3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Ciona intestinalis"
/db_xref="taxon:7719"
/Clone="034ZA11"
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779.50
76.25%
55.94%
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 ----CAGAACAGGGGA--- 215
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                 source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ArgGlnLysGlnLeuLeuAsnGlnArgPheGluThrLeuCysAlaValLeuGluGluArg 227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAACATGAAGAAGAAAGTGAATATTTACTGCGTGACTTGTCAGAAACCAACGTGTTCT 452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lee, N.H., Glodek, A., Chandra, I., Mason, T.M., Quackenbush, J., Kerlavage, A.R. and Adams, M.D.
Rat Genome Project: Generation of a Rat EST (REST) Catalog &
                                                                                                                                                                                                                                                                                                                                                                                                         EST189742 Normalized rat heart, RHEAM89 3' end, mRNA sequence.
                                                                            9712, Medical Center Drive, Rockville, Tel: (301)-838-3529
Fax: (301)-838-0208
                                                                                                                                                                                                                                                                                    Eukaryotā; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                       Rattus sp
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                                                                                                                                                                  Unpublished (1998)
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                                                                                                                                   The Institute for Genomic Research
                                                                                                                                                   Contact: Lee,
                                                                                                                                                                                     Gene
                                                                                                                                                                                                                                                                       Rattus
                                                                                                                                                                                                                                                     (bases 1 to 638)
                                              il: nhlee@tigr.org
primer: M13-21.
/organism="Rattus sp.
                 Location/Qualifiers
1. .638
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Best Local Similarity:
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                    TITLE
      JOURNAL
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                                                                                                                                                                                                                                                                         ArgLeuAspValProGluGlySerGlyLeuHis 366
                                                                                                                                                                                                                                                                                                  GAAGAGGATGACGAGGTGACTTTGGACGGGGAAGAGGGCAACACAGGGCTGGAGGAGGAG
                                                                                                                                                                                                                                                   CGGCTGGACGGGCCAGAA-----GGTTTGCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Expressed genes in X. laevis embryo Unpublished (2001)
                                                                                                                                                                   BJ059953 MIBB Mochii normalized Xenopus tailb laevis cDNA clone XL064904 5', mRNA sequence.
                                     Kitayama, A., Terasaka, C., Mochii, M., Ueno, N.,
                                                                                                    African clawed frog.
Xenopus laevis
                                                    Xenopodinae; Xenopus.

1 (bases 1 to 628)
                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Amphibia; Battachia; Anura; Mesobatrachia; Pipoidea;
                                                                                                                                                 вл059953.1
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Site_2: NotI"
a 221 c 165 g
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/db_xref="taxon:10118"
/db_xref="taxon:10118"
/clone="Repam89"
/clone=lib="Normalized rat heart, Bento Soares"
/note="Organ: heart; Vector: pT7T3Pac; Site_1: EcoRI;
                                                                                                                                                GI:17496683
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778.00
94.15%
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Indels:
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                                                                           Pipoidea;
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                                     Shin-i, T.
                                                                        Euteleostomi;
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Best Local Similarity:
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                           241 GluLysLeuGlnArgValArgGlyLeuIleArgGlnTyrGlyAspHisLeuGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 LeuTrpGlnSerArgGlySerThrThrValSerSerGlyGlyArgPheArgCysProSer :::::: ::::||||||||
GAAAGGCTTGAATATGTCCGATCATTAATGAAAAAATATGGCAGCCACACGGAG
                                                              TATGCTATTTTGGAACAAAGAAAGGGGGAACTGAGCCAAGCAATCACCAGAGACCAAGAA
                                                                               CysAlaValLeuGluGluArgLysGlyGluLeuLeuGlnAlaLeuAlaArgGluGlnGlu 240
                                                                                                                                                  ThrIleGluAspAsnSerArgArgGlnLysGlnLeuLeuAsnGlnArgPheGluThrLeultl:::|||::::|||:::
                                                                                                                                                                                                                             LeuValAlaGlyAsnAspArgValGlnAlaValIleThrGlnMetGluGluValCysGln
                                                                                                                                                                                             CTGGTTGGATGTAATGACAGAATTCAGGCAGTAGTAAGCCAACTGGAGGAGACTTGCAAA
                                                                                                                                                                                                                                                             GCTCCTCTTACACAAGTTTTCCCAAAGACAAAGTCTGAAACTCTCAGATGGCATTGCAATA
                                                                                                                                                                                                                                                                                    AlaProLeuProThrIleTyrLysArgGlnLysSerGluLeuSerAspGlyIleAlaMet
                                                                                                                                                                                                                                                                                                                            TGTGAAGTTCCTACCTGCTCCATGTGCAAAGTGTTTGGAGCTCACAAAAATTGTGAGGTT
                                                                                                                                                                                                                                                                                                                                                CysGluValProThrCysSerLeuCysLysValPheGlyAlaHisLysAspCysGluVal
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                                                                                                                              ACCGTTGAGGAAAATAGTAAAAGGCAAAAAAGAACAACTATGTGAACAATTTGATTATCTG
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Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="whole embryo"
/dev_stage="stage 25"
/note="Vector: pBSRN3; Site_1: NotI; Site_2: EcoRI; cDNAs
were oligo-dT primed and directionally cloned. Staging
according to Nieuwkoop and Faber. Library is subtracted
and was constructed by N. Garrett and A.M. Zorn,
(Wellcome/CRC Institute). "
a 111 c 151 g 149 t
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/clone="XL064g04"
/clone_lib="NIBB Mochii normalized Xenopus
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RESULT 14
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                                                                                  312
                                                                                                                                                                                       41 ProCysGlnHisAsnLeuCysArgLysCysAlaAsnAspValPhe------GlnAl
                                                                                                                                                                                                                                                                                      21 GluLysGlnLeuIleCysProIleCysLeuGluMetPheSerLysProValValIleLeu 40
                                           77
                                                                                                                                                                                                                                                                                                                                                                      1 MetAsnPheThrValGlyPheLysProLeuLeuGlyAspAlaHisAsnMetAspAsnLeu
CTCTAACCCGTATTTGCCCCACAAGAGGAGGTACCACCATGGCATCAGGGGGCCGATTCCG
                                                                                                                        aSerAsnProLeuTrpGlnSerArgGlySerThrThrValSerSerGlyGlyArgPheAr 77
                                                                                                                                                                 CCTTGTCAGCACAACCTGTGTAGGAAATGTGCCAGTGATATTTTCCAGGCAAGAACAGGC
                                                                                                                                                                                                                                                                                                                                 ATGAGCGCATCTCTGAATTACAAATCTTTTTCCAAAGAGCAGCAGACCATGGATAACTTA
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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/clone=lib="NIH_MGC.89"
/clone=lib="NIH_MGC.89"
/tissue_type="hypernephroma, cell line"
/tissue_type="hypernephroma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: kidney: Vector: pCMV-SPORT6; Site_1: NotI;
/note="Organ: kidney: Vector: pCMV-SPORT6; Site_1: NotI;
/site_2: Sall; Cloned unidirectionally; oligo-dT primed.
site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.3 kb Library enriched for
full-length Clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
a 288 c 291 g 207 t
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BF284900 608 bp mRNA linear EST 28-NOV-20
EST449491 Rat Gene Index, normalized rat, Rattus norvegicus cDNA
Rattus norvegicus cDNA clone RGIEX57 3' sequence, mRNA sequence.
                                                                                                                                                                                                                                             Email: nhlee@tigr.org
This clone is available through the ATCC,
tel#703-365-2700 for further information.
                                                                                                                                                                                                                                                                                                     The Institute for Genomic Research 9712, Medical Center Drive, Rockvi. Tel: (301)-838-3529
Fax: (301)-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2000)
Other_ESTs: EST350057
                                                                                                                                                                                                                                                                                                                                                                                                                                    Malek,R.L., Cho,J., Lee,Y., Karamycheva,S., Parvizi,B., Pertea,G., Sultana,R., Tsai,J., White,J., Quackenbush,J. and Lee,N.H. Generation of ESTs from Normalized Rat Embryo, Bento Soares
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   101
   מ
/note-"Vector: pT3T7Pac; Site
Combination of ROV, RBR, RKI,
, RHE, RPC, RPM"
, RHE, RPC, RPM"
                                                                                                           norvegicus cDNA"
                                                                     /tissue_type="mixed tissue"
/lab_host="DH5-alpha"
                                                                                                                                                   /organism="Rattus norvegicus"
/db_xref="taxon:10116"
/clone="RGIEX57"
                                                                                                                                 /clone_lib="Rat Gene Index, normalized
                                                                                                                                                                                                                           location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                               Rockville, MD 20850, USA
                                                         Site_1: EcoR1;
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                                         Site_2: Not1;
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495 bp mRNA linear EST 07-FEB-2002 pgm2n.pk008.d8 Normalized Chicken Breast Muscle, Leg Muscle, and Epihhyseal Growth Plate cDNA library (pgm2n) Gallus gallus cDNA clone pgm2n.pk008.d8 5' similar to ref|NP_067422.1 (NM_021447) muscle-specific RING-finger protein; 4930486E09Rik [Mus musculus] pb|AAG03076.1| (AF294790) RING-finger protein MURF [Mus musculus],
Unpublished (2002)
Contact: Larry A. Cogburn
University of Delaware
                                                                  1 (bases 1 to 495)
Cogburn,L.A. and Monsonego-Ornan,E.
ESTs from Normalized Chicken Breast
                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves; Neognathae; Galliformes; Phasian: Phasianinae; Gallus.
                                                                                                                                                      Gallus gallus
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                                               icken Breast Muscle, Leg Muscle, and cDNA library, USDA/IFAFS Animal Genome
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Tetraodon
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Tel: 302-831-335
Fax: 302-831-282
Email: cogburn@udel.edu, www.chickes
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="Breast muscle, leg muscle and growth plate" \label{eq:problem}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:9031"
/Clone="pgm2n.pk008.d8"
/Clone=lib="Normalized Chicken Breast Muscle, Le
/clone_lib="Normalized Chicken Breast Muscle, Le
and Epiphyseal Growth Plate cDNA library (pgm2n)
/sex="Male and Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /strain="Commercial broiler and Strains 90 & 21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /dev_stage="Breast,leg:Embryo(d19);post-hatch(1d,1,3,5,7,9,11 weeks);growth plate(1d,7d,14d post-hatch)"
/lab_host="E. coli EMDH10B"
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                                   ArgAsnLeuLeuValGluAsnIleIleAspIleTyrLysGlnGluSerSerArgProLeu 116
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                                                                                                                                                                                   AlaSerAsnProLeuTrpGlnSerArgGlySerThrThrValSerSerGlyGlyArgPhe 76
                                                                                                                                                                                                                             CGCTGTCCTACCTGCCGCTTTGAAGTTGTCCTTGACCGCCACGGTGTGCACGGGCTGCAG
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/note="Genoscope sequence ID : COBG108DA02LP1-end : 300 c 312 g 196 t 4 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 HisAlaLysAlaGluGlnHisLeu-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   746 TGCAAGGTCTTTGGCCAGCACAAAGACTGCGAGGTTGCCACTTTACCGGCTGTTTACGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               985
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1092)
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Plate: LLCM1838 row: n column:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1999)
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National Institutes of Health, Mammalian Gene Collection (MGC)
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/tissue_type="riabdomyosarcoma"
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/note="Organ: muscle; Vector: pOTB7; Site_1: ECORI;
/note="Organ: muscle; Vector: pOTB7; Site_1: ECORI;
/note="Organ: made by oligo-dT priming."
Site_1: ECORI;
/note="Organ: made by oligo-dT priming."
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/clone="IMAGE:5020997"
/clone_lib="NIH_MGC_17"
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Best Local Similarity:
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                                                       279 yrLeuGlnGlnAlaLysGluLeuIleAsnLysValGlyAlaMetSerLysValGluLeuA 299
299 laGlyArgProGluPro 304
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                                                                                                                                                                                        239 lnGluGluLysLeuGlnArgValArgGlyLeuIleArgGlnTyrGlyAspHisLeuGluG
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                                                                                                                                                                                                                                                                                                                                                                                                                                         160 ValAla-ProLeuProThrileTyrLysArgGlnLysSerGluLeuSer-AspGlyIleA 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   374 TGTAGACATGAAGTGGTTTCGGATAGACATGGGGTATATGGACTTCAGAGGAACCTGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            134
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                        ACAGGAAACCAGCCCACGACGCCCAACAGCGACAGCAAACGTGCAACGCCCACACCTGC 986
                                                                                       AGGGCAGTCCGACCTAGGAC-------GACCGTCCACAAGAGGCGAGAA 926
                                                                                                                      lySerSerLysLeuValGluSerAlaIleGlnSerMetGluGluProGlnMetAlaLeuT 279
                                                                                                                                                          AGCCACACCCAACCCAAACACAAAGGAAGGAACGAGACGC------GACCACAACAAAC
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                                                                                                                                                                                                                                                                                                                                                        GCATACTCGTGGGCAGCAACGACCGAGTACAGGGAGTGATCAAGCAGCTGGAAAACACCT
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                                  LeuTrpGlnSerArgGlySerThrThrValSerSerGlyGlyArgPheArgCysProSer
                                                                                                                              CCTTGTCAGCACAACCTGTGTAGGAAATGTGCCAGTGATATTTTCCAGGCCTCTAACCCG
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Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 776)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
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/tissue_type="rhabdomyosarcoma"
/tissue_type="rhabdomyosarcoma"
/tissue_type="rhabdomyosarcoma"
/note="Organ: muscle; Vector: pOTB7; Site_1: ECORI;
/note="Organ: muscle; Vector: potential"
/note="Organ: muscle; Vector: pOTB7; Site_1: ECORI;
/note="Organ: muscle; Vector: potB7; Site_1: potB7; Site_1: potB7; Site_1: potB7; Site_1: potB7; Site_1: potB
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                                                                                                                                                                                                                                                                                                             Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6855 Fax: 81-559-81-6855
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                           Contact: Tadasu Shin-i
                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kitayama,A., Terasaka,C., Mochii,M.,
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1 (bases 1 to 552)
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                                                               a
                                                          /tissue_type="whole embryo"
/dev_stage="stage 25"
/dev_stage="stage 25"
/note="wector: pBSRN3; Site_1: NotI; Site_2: EcoRI; cDNAs
were oligo-dT primed and directionally cloned. Staging
according to Nieuwkoop and Faber. Library is subtracted
and was constructed by N. Garrett and A.M. Zorn,
(Wellcome/CRC Institute). "
109 c 123 g 145 t 1 others
                                                                                                                                                                                                                   /organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="XL098g02"
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ALIGNMENTS

RESULT 1 AA800245/c COMMENT REFERENCE SOURCE ORGANISM FEATURES KEYWORDS VERSION ACCESSION DEFINITION LOCUS JOURNAL TITLE AUTHORS source AA800245
EST189742 Normalized rat heart,
RHEAM89 3' end, mRNA sequence. Contact: Lee, NH
The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
7el: (301)-838-3529
Teax: (301)-838-0208
Email: nhlee@tigr.org
Seq primer: M13-21. 1 (bases 1 to 638)
Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
Kerlavage,A.R. and Adams,M.D. Rattus sp. EST AA800245 Unpublished (1998) Gene Index Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus sp. AA800245.1 GI:2863200 Rattus. Location/Qualifiers
1. .638 /organism="Rattus sp." mRNA linear EST 30-APR-1998 Bento Soares Rattus sp. cDNA clone

Result

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.

Score

Match Length DB ID

9

AA800245 BF284900 AK019655 BF855618 BM030114 Query

0 0

538.2 508.2 482.4

37.6 35.5 33.7 31.0 30.7 29.4

638 608 485 555 516 461

> AA800245 EST189742 BF284900 EST449491 AK019655 Mus muscu BF855618 RCO-FN020 BM030114 488634 MA

Description

AV006036 AV006036

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                                                                                                                                                EST449491 Rat Gene Index, normalized rat, Rattus norvegicus cDNA Rattus norvegicus cDNA clone RGIEX57 3' sequence, mRNA sequence.
    Malek, R.L., Cho, J.,
                                              Mammalia; Eutheria;
                                                            Eukaryota; Metazoa;
                                                                             Rattus norvegicus
                                                                                                                EST
                                                                                                                           BF284900.1 GI:11215970
                                                                                                                                             BF284900
                                   Rattus.
                                                                                              Norway rat.
                 (bases 1 to 608)
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/note="Organ: heart; Vector: pT7T3Pac; Site_1: EcoRI;
Site_2: NotI"
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/db_xref="taxon:10118"
/clone="RHEAM89"
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91.7%;
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                                                           Chordata;
                                                Rodentia;
 Lee,Y.,
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Pred. No. 2.4e-107;
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Karamycheva, S.,
                                        Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae;
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1413 TAAAGGACTCAAGTGTCCC
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                            ATCTGCGCAGAGACCATCGCGCTACCCATCTCGGCCTCCACCCCCAGGGATGGTTCTCAA
                                                            ATCTGCGCAGAGACCACCGCGCCACCAAGCTCGGCTTCCCGGCCCCGGGGAAGGTTCTCAA 1412
                                                                                                            GCACTGATCCGACTCTGATCCAGAGCGCACGCC----
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                                                                                                                                                                                                                                                                                                                       GCACTGACCCGACTCTGATCCAGAGCGCACACCCGAAGCGGAGCCCAAGGGATGCTGAGG 1352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTCCGCCATCCAGGCAGGAGGCCGCAGATGGCTCTCTACCTCCAGCAGGCCAAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTCCGCCATCCAGTCCATGGAGGAGCCGCAGATGGCTCTCTACCTCCAGCAGGCAAAGGA 1052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGTGCGTAGCCTCATCCGCCAGTACGGAGACCACTTGGAGGCCTCCTCTAAGCTGGTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9712, Medical Center Drive, Rockville, MD Tel: (301)-838-3529
Fax: (301)-838-3529
Email: nhlee@tigr.org
This clone is available through the ATCC, tel#703-365-2700 for further information.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sultana,R., Tsai,J., White,J., Quackenbush,J. and Lee,N.H. Generation of ESTs from Normalized Rat Embryo, Bento Soares Unpublished (2000)
Other_ESTs: EST350057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Lee,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The Institute for Genomic Research
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a 207 c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="mixed tissue"
/lab_host="DH5-alpha"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Rat Gene Index, normalized rat, Rattus
norvegicus cDNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Rattus norvegicus"
/db_xref="taxon:10116"
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RESULT 3
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                                                                                                                                            PUBMED
                                                                                                                                                                                                                                                                                                RS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Alzawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Salto,T., Colobori,T., Bono,H., Kasukawa,T., Saito,R., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Kedota,K., Matsuda,H., Stauklido,I., Pesole,G., Color, Kochiwa,H., Kondo,H., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fleicher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schombach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Wand,H., Washira,H., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S., and Havashiraki,Y. Oshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shibata, K., Itoh, M., Alzawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A., Arakawa,T., Baldarelli,R., Bono,H., Brownstein,M., Bult,C., Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T.,
                                                                                                                                                                                                       Functional annotation of a full-length mouse cDNA collection Nature 409 (6821), 685-690 (2001)
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                                                                                                                                                                                                                                                                                     and Hayashizaki,Y.
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COMMENT
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                      1066 GTCGGGGCAATGTCGAAGGTGGAGCTGGCAGGACGGCCGGAGCCAGGCTATGAGAGCATG 1125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                 1006 TCCATGGAGGAGCCGCAGATGGCTCTCTACCTCCAGCAGGCAAAGGAGCTGATCAACAAG 1065
                                                                                                                                                                                                            946 ATCCGCCAGTACGGAGACCACTTGGAGGGCTCCTCAAAGCTGGTGGAGTCCGCCATCCAG 1005
                                                                  62 TCCATGGAGGAGCCGCAGATGGCTCTACCTCCAGCAGGCAAAGGAGCTGATCAACAAG 121
                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                2 ATCCGCCAGTACGGAGACCACTTGGAGGGCTCCTCAAAGCTGGTGGAGTCCGCCATCCAG
Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hiraoka, T., Hori, F., Hume, D., Imotani, K., Ishil, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawal, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Schrimi, L., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yamanaka, I., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and
                                                                                                                                                                                                                                                             483;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (18-AUG-2000) Yoshihide Hayashizaki, The Institute of physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Please visit our web site (http://genome.gsc.riken.go.jp/) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hayashizaki,Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BamHI. Host: DH10B
                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                              evidence: 130 ring finger protein 30 r/db_xref="MGD: MGI:1889623" /db_xref="MGD: MGI:1889623" 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="FANTOM_DB:4930486E09"
/db_xref="MGD:MGI:1912089"
                                                                                                                                                                                                                                                                                                                                                                                                                                            evidence: ISS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="testis"
/clome_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="data source:MGD, source key:MGI:1889623,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="Rnf30"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAGCAATTCTCTGTGAGCGTGGAGCACGTGGCCGAAATGTTGCGAACCATCGACTTCCAG 1185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCGGGCGCCGCTGGGGATGAAGAGGATGACGACATGGCTTTGGATGGGGAGGAGGAGGAAAT 301
                                                                                                                                                                                                                                         Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=RcO&t2=RCO-FNO2O4-
161100-031-d06&t3=2000-11-16&t4=1)
Seq primer: puc 18 forward
                                                                                                                                                                                                      High quality sequence start: 51 High quality sequence stop: 120.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                      Tel: +55-11-2704922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Simpson A.J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence tags
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1. (bases 1 to 555)
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RCO-FN0204-161100-031-d06 FN0204 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                             Prof. Antonio Prudente 109, 4 andar, 01509-010,
                                                                                                                                                                                                                                                                                                                                                                                      +55-11-270700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Natl. Acad. Sci. U.S.A.
/note-"Organ: prostate_normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent
                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="FN0204"
                                                                                                                                                                                  Location/Qualifiers
                                                                      /dev_stage="Adult"
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RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            456 CCTGGACAGGCATGGTGTCTATGGCCTGCAGCGGAACCTGCTAGTGGAGAACATCATTGA
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                                                                                                                                         Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T., Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G., Pertea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and Keele,J.W.
                                         Contact: Smith TPL
                                                                21180013
                                                                             Genome Res. 11 (4), 626-630 (2001)
                                                                                                Sequence evaluation of four pooled-tissue normalized libraries and construction of a gene index for cattle
                                                                                                                                                                                                                                                              Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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  DA, ARS, US Meat Animal Research
Box 166, Clay Center, NE 68933-(
                                                                                                                                                                                                                                         (bases 1 to 516)
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Pred. No. 1.5e-86;
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                                                                                                                                                                                                                                                                                                                                                                            889 CTGCTTCAAGCACTGGCCCGGGAGCAGGAGGAGAGTTGCAGCGCGTGCGGGGCCTCATC
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                                                                                                                                                                                   CGCCAGTACGGAGACCACCTGGAGGCCTCCTCTAAGCTGGAGTCTGCCATCCAGTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: smith@email.marc.usda.gov Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plate: 116 row: J column: 19 Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FORWARD: AGGAAACAGCTATGACCAT
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             461 bp
AV006036 Mus musculus C57BL/6J h
1020004I19, mRNA sequence.
AV006036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sal1; Library made from pooled tissue from testis, thymus, semitendonosus muscle, longissimus muscle, pancreas, adrenal, and endometrium."

a 137 c 171 g 89 t
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/db_xref="taxon:9913"
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="MARC 2BOV"
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90.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches 48; Indels
                                                                heart Mus musculus cDNA clone
                                                                                    mRNA
                                                                                      linear
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                                                                                      EST 25-AUG-1999
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                                                                                                                                                                                                                                                                                                                     1029 TCTCTACCTCCAGCAGGCAAAGGAGCTGATCAACAAGGTCGGGGCAATGTCGAAGGTGGA 1088
1209 GGATGACGACATGGCTTTGGATGGGGAGGAGGGCAATGCGGGGCTGGAGGAGGAGCGGCT 1268
                                                                                                    1149 GCACGTGGCCGAAATGTTGCGAACCATCGACTTCCAGCCGGGCGCCGCTGGGGATGAAGA 1208
                                                                                                                                                                                        1089 GCTGGCAGGACGGCCGAGCCAGGCTATGAGAGAGCATGGAGAGCAATTCTCTGTGAGAGCGTGGA 1148
                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                   TTTNTACTTCCAGCNGGCANAGGAGCTGATCAACAAGGTCGGGGCAATGTCGAA-GTGGA 119
                                                                                                                                                            CCTGCCACGACGCCGGAGCCAGG-TATGAGAGCATGGAGCAATTCTCTGTGAGCGTGGA 178
                                                       GCACGTGGCCGAAATGTTGCGAACCATGGACTTCCAGCCGGGCGCCGCTGGGGATGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K., Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Fundyama, T., Hara Akahira, S., Akiyama, J., Fushidawa, T., Itoh, M., Izawa, M., Kawai, J., Kikuchi, N., Kojima, Y., Matsuyama, T., Niitsuma, H., Oda, H., Owa, C., Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara Y., Suzuki, H., Tateno, M., Tomaru, Y., Tominaga, N., Watanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 461)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thermostabilization and thermostavation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998)) using RNA pranscriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998)) please visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
Contact: Chie Owa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RIKEN Mouse ESTs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genome Science Laboratory
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                adaptors (Pharmacia), digested with Not I and cloned in
the Not I and Eco RI sites of the modified pT/T3 vector
RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Mus musculus C57BL/6J heart"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:10090"
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) with a modified polylinker; Site_1: Not I; Site_2: Eco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="heart
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism-"Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       th a modified polylinker; Site_1: Not I; Site_2: Eclst strand cDNA was primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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Pred. No. 9.7e-82;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 9; Length 461;
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            Matches 465;
                         Query Match
Best Local Similarity
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RCO&t2=RCO-FNO204-
161100-031-e06&t3=2000-11-16&t4-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence start: 42 High quality sequence stop: 512.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: +55-11-2704922
Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 512)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jogeneel,C.V., O'Hare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 512 bp mRNA linear EST 16-JAN-200 RCO-FN0204-161100-031-e06 FN0204 Homo sapiens cDNA, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                             primer: puc 18 forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-Sp
        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
                                                                                              //note="Organ: prostate_normal; Vector: puc18; Site_1: SmaI
; Site_2: SmaI; A min1-library was made by cloning
products derived from ORESTES PCR (U.S. Letters Patent
application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the pUC 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions."
a 138 c 157 g 113 t
                                                                                                                                                                                                                                                              /db_xref="taxon:9606"
/clone_lib="FN0204"
/dev_stage="Adult"
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                       29.1%;
91.0%;
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                       Score 416.2; DB
Pred. No. 1e-80;
    Mismatches
                                       DB 12;
  43; Indels
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                                                                                                                                                                                                                                                                        Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
                                                                                                                                                                                                                                                                                                                                                              Expressed genes in X. laevis embryo Unpublished (2001)
Contact: Tadasu Shin-i
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                                                                                                                                                                                                                  Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                       Kitayama, A., Terasaka, C., Mochii, M., Ueno, N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus.

1. (bases 1 to 595)
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/note="Vector: pBSRN3; Site_1: NotI; Site_2: EcoRI; cDNAs
were oligo-dT primed and directionally cloned. Staging
                                                                                                                                   /organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="XL095b10"
                                                 /tissue_type="whole embryo"
/dev_stage="stage 25"
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                       Akimura, T., Arakawa, T., Carninoi, P., Furuno, M., Hanagaki, T., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii, Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Saito, R., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Watahiki, A., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y., Tayara, Shiraki, A., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y., Tayara, Shiraki, A., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y., Tayara, Shiraki, A., Muramatsu, M., and Hayashizaki, Y., Tayara, Shiraki, A., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y., Tayara, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BB732046 BTKEN full-length enriched, 12 days embryo whole body Musmusculus cDNA clone E970020A01 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 432)
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RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al.
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81.7%;
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Best Local :
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                                                                                         999 CATCCAGTCCATGGAGGA-GCCGCAGATGGCTCTCTACCTCCAGCAGGCAAAGGAGCTGA 1057
                                                                                                                                                                                                                                    Local Similarity
1 CATCCAGTCCATGGAGGAGGCCGCAGATGGCTCTCTACCTCCAGCAGGCAAAGGAGCTGA 60
                                                                                                                                                                                                 427;
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URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
Carninci,P., Shibata,Y., Muramatsu,M. and Hayashizaki,Y.,
M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.,
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (200)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
Watahiki,M., Yoneda,Y., Muramatsu,M., Inoue,Y., Kira,A. and
S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
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The Institute of Physical and Chemical Research (RIKEN)
The Institute of Physical and Chemical Research (RIKEN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2001)
Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hayashizaki,Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                            williage body "/tissue_type="whole body" //tissue_type="whole body" //dev_stage="12 days embryo" //dev_stage="12 days ext of 15,247 clones from 11 embryo clone is among a rearrayed set of 15,247 clones from 11 embryo cDNA libraries (including preimplantation stage embryos from unfertilized egg to blastocyst, embryonic part of E7.5 embryos, extraembryonic part of E7.5 embryos, and E12.5 female mesonephros/gonad) and one newborn ovary cDNA library. Average insert size 1.5 kb. All source libraries are cloned unidirectionally with Oligo(dT)-Not primers. References include: (1) Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray, 2000, proc. Natl. Acad. Sci. U S A, 97: 9127-9132; (2) Proc. Natl. Acad. Sci. U S A, 97: 9127-9132; (2) Proc. Natl. Acad. Sci. U S A, 97: 9127-9132; (2) Proc. Natl. Acad. Sci. U S A, 97: 9127-9132; (2) Proc. Natl. Acad. Sci. U S A, 97: 9127-9132; (2) Proc. Natl. Acad. Sci. U S A, 97: 9127-9132; (2) Proc. Natl. Acad. Sci. U S A, 97: 9127-9132; (2) Proc. Natl. Acad. Sci. U S A, 97: 9127-9132; (2) Proc. Natl. Acad. Sci. U S A, 97: 9127-9132; (2) Proc. Natl. Acad. Sci. U S A, 97: 9127-9132; (2) Proc. Natl. Acad. Sci. U S A, 97: 9127-9132; (2) Proc. Natl. Acad. Sci. U S A, 97: 9127-9132; (2) Proc. Natl. Acad. Sci. U S A, 97: 9127-9132; (2) Proc. Natl. Acad. Sci. U S A, 97: 9127-9132; (2) Proc. Natl. Acad. Sci. U S A, 97: 9127-9132; (2) Proc. Natl. Acad. Sci. U S A, 97: 9127-9132; (2) Proc. Natl. Acad. Sci. U S A, 97: 9127-9132; (2) Proc. Natl. Acad. Sci. U S A, 97: 9127-9132; (2) Proc. Natl. Acad. Sci. U S A, 97: 9127-9132; (2) Proc. Natl. Acad. Sci. U S A, 97: 9127-9132; (2) Proc. Natl. Acad. Sci. U S A, 97: 9127-9132; (2) Proc. Natl. Acad. Sci. U S A, 97: 9127-9132; (2) Proc. Natl. Acad. Sci. U S A, 97: 9127-9132; (2) Proc. Natl. Acad. Sci. U S A, 97: 9127-9132; (2) Proc. Natl. Acad. Sci. U S A, 97: 9127-9132; (
                                                                                                                                                                                            Conservative
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/clone="E970020A01"
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/strain="C57BL/6J"
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                                                                                                                                                                                                                                         28.9%;
98.8%;
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                                                                                                                                                                                                                                              Score 413.6; DB 1
Pred. No. 3.5e-80;
                                                                                                                                                                                                      Mismatches
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TITLE
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                                                                                                                                                                                                                                                   Email: msoares@blue.weeg.uiowa.edu
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to verify it as a clone from the normalized AV canal at 15 dpc library cDNA Library Preparation. M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com)
                                                                                                                                                                                                                               Seq primer: M13 Forward POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   451 Eckstein Medical Research Building Iowa City,
Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Program for Rat Gene Discovery and Mapping University of Iowa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Soares, MB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AI712700 504 bp mRNA linear EUI-R-AF1-aau-e-02-0-UI.sl UI-R-AF1 Rattus norvegicus UI-R-AF1-aau-e-02-0-UI 3', mRNA sequence.
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Rattus norvegicus
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                                                                    /strain="sprague-Dawley"
/db_xref="taxon:10116"
/clone="UJ-R-AF1 aau-e-02-0-UI"
/clone_lib="UI-R-AF1"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                                                  /dev_stage="adult"
                                                                                                                                                        /organism="Rattus norvegicus"
                                                                                                                                                                                                      Location/Qualifiers
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                                               1414 AAAGGACTCAAGTGTCCC 1431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           504 GTGCGTAGCCTCATCCGCCAGTACGGAGACCACTTGGAGGCCTCCTCTAAGCTGGTGGAG 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          934 GIGCGGGGCCTCATCCGCCAGTACGGAGACCACTTGGAGGGCTCCTCAAAGCTGGTGGAG 993
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                                                                                                                                      TCTGCGCAGAGACCACCGCGCCACCAAGCTCGGCTTCCCGCCCCCGGGAAGGTTCTCAAT 1413
                                                                                                                                                                                                                   CACTGACCCGACTCTGATCCAGAGCGCACACCCGAAGGGGAGCCAAGGGATGCTGAGGA 1353
                                                                                                                                                                                                                                                                                       GAAGAGGGCAACACAGGGCTGGAGGAGGAGCGGCCTGGACGGGCCAGAAGGTT-----TG 151
AAAGAACTCATGTGTCCC 18
                                                                                                                                                                                                                                                                                                                     GAGGAGGCAATGCGGGGCTGGAGGAGGAGGAGGTGGACGTGCCAGAAGGCTCAGGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCCGCCATCCAGTCCATGGAGGAGCCGCAGATGGCTCTCTACCTCCAGCAGGCCAAGGAG
                                                                                         TCTGCGCAGAGACCATCGCGCTACCCATCTCGGCCTCCACCCCAGGGATGGTTCTCAAT
                                                                                                                                                                                                                                                                                                                                                                                            ATCGACTTCCAGCCGGGCGCCTCTGGGGATGAAGAGGATGACGAGGTGACTTTGGACGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TATGAGAGCATGGAGCAATTCTCTGTGATCGTGGAGCACGTGGCGGAAATGTTGCGGACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAG_TISSUE=AV canal at 15 dpc TAG_SEQ=GAAGG"
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91.2%;
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REFERENCE KEYWORDS VERSION ACCESSION DEFINITION ORGANISM AUTHORS Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 392)
Carninci,P., Shibata,K., Ozawa,Y., Konno,H., Itoh,M., Aizawa,K., Akihira,S., Akiyama,J., Fukuda,S., Fukunishi,Y., Funayama,T., Hara,A., Hayatsu,N., Hori,F., Ishikawa,T., Itoh,M., Izawa,M., Kawai,J., Aikuchi,N., Kojima,Y., Matsuyama,T., Niitsuma,H., Oda,H., Owa,C., Sato,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara Mus musculus AV006120 Mus musculus C57BL/6J heart Mus musculus cDNA clone AV006120.1 GI:4782970 1020006G17, mRNA sequence. nouse mouse.

EST 25-AUG-1999

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                                                                                                                                                                                                                                                                                                                                                                                                                                                         1162 ATGTTGCGAACCATCGACTTCCAGCCGGGGCGCCGCTGGGGATGAAGAGGATGACGACATG 1221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1102 CCGGAGCCAGGCTATGAGAGCATGGAGCAATTCTCTGTGAGCGTGGAGCACGTGGCCGAA 1161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1042 CAGGCAAAGGAGCTGATCAACAAGGTCGGGGCAATGTCGAAGGTGGAGCTGGCAGGACGG 1101
                                                                                                                                                                                                                                                                    1282 GGCTCAGGCCTGCACTGACCCGACTCTGATCCAGAGCGCACACCCCGAAGCGGGAGCCAAG 134:
                                                                                                                                                               1342 GGATGCTGAGGATCTGCGCAGAGACCACCGCGCCCACCAAGCTCGGCTTCCCGCCCCCGGG 1401
                                                                                                                                                                                                                                                                                                                          183 GCTTTGGATGGGAGGAGGGCAATGCGGGGNTGGAGGAGGAGCGGTTGGACGTGCCAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                              123 ATGTTGCGAACCATNGACTTCCAGCCGGGCGCCGCTGGGGATGAAGAGGATGACGACATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCGGAGCCAGGCTATGAGAGCATGGAGCAATTNTCTGTGAGCGTGGAGCANGTGGCCGAA 122
                                           AAGGTTCTCAATAAAGGACTCAAGTGTCCC 1431
                                                                                                                                                                                                                      AAGGTTCTCAATAAAGGACTCAAGTGTCCC 392
                                                                                                                    GGATGCTGAGGATNTGCGCAGAGACCACCGCGCCCACCAAGNTCGGCTTCCCGCCCCCGGG
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Thermostabilization and thermoactivation of thermolabile enzymes by
Thermostabilization and thermoactivation of thermolabile enzymes by
Trehalose and its application for the synthesis of full length cDNA
(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
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Tel: 81-298-36-9145
Fax: 81-298-36-9098
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Chie Owa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector {\tt T}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia ) with a modified polylinker; Site_1: Not I; Site_2: Eco RI: 1st strand cDNA was primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:10090"
/clone="1020006G17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Mus musculus C57BL/6J heart"
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95.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 361.2; DB 9; Length 392; Pred. No. 9.7e-69; O; Mismatches 15; Indels 1
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                                                                                                                                                                                                                  Matches 409;
                                                                                                                                                                                                                                           Best Local
                                                1040 AGCAGGCAAAGGAGCTGATCAACAAGGTCGGGGCAATGTCGAAGGTGGAGCTGGCAGGAC 1099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
                                                                                                                                     980 CAAAGCTGGTGGAGTCCGCCATCCAGTCCATGGAGGAGCCGCAGATGGCTCTCTCACCTCC 1039
                                                                                                         456 CTAAGCTGGTGGAGTCCGCCATCCAGTCCATGGAGGAGCCGCAGATGGCTCTCTACCTCC
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized AV canal at 16.5 dpc library CDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BE099923 456 bp mRNA linear FULL-R-BJ1-atl-f-12-0-UI.Sl UI-R-BJ1 Rattus norvegicus UI-R-BJ1-atl-f-12-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          451 Eckstein Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 8250
Fax: 319 335 9565
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seq primer: M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: msoares@blue.weeg.uiowa.edu
                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 456)
                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                       73 a
                                                                                                                                                                                                                                                                                                                                                                                                                        /note="vector: pT/T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-BJ1 library is a subtracted library derived from the following tissues: atrium at 16.5 dpc, ventricle at 16.5 dpc, AV canal at 16.5 dpc, atrium at 15 dpc, ventricle at 15 dpc, AV canal at 15 dpc, atrium at 15 dpc, and adult heart. AV canal at 15 dpc, ventricle at 13 dpc, and adult heart. For a detailed description of the library from which this clone was derived, please visit our web site at ratest.eng.uiowa.edu. The subtraction has been previously described in (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)
TAG_ILB-UI-R-JJ1
                                                                                                                                                                                                                                                                                                                                                                              TAG_SEQ=GAACC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="Sprague-Dawley"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                       TAG_TISSUE=AV canal at 16.5 dpc
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/lab_host="DH10B (Life Technologies)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="UI-R-BJ1-at1-f-12-0-UI"
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                                                                                                                                                                                                                                                                                                                                                          153 c
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                                                                                                                                                                                                                                           25.2%;
                                                                                                                                                                                                                    0;
                                                                                                                                                                                                               Score 360; DB 10; Length 456; Pred. No. 1.9e-68; 0; Mismatches 30; Indels 1
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                                                                                                                                                                                                                                                                                                                                   DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAMIL1483 row: j column: 15
High quality sequence start: 25
High quality sequence stop: 890.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
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1. (bases 1 to 912)
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              /note-"Organ: brain; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: ECORV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-3 kb Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Note: a 232 c 266 g 178 t
                                                                                                                                                                                                                                         /clone="IMAGE:5193326"
/clone_lib="NIH_MGC_114"
                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                        /lab_host="DH10B"
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                Bonaldo, M.F., Lenno
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UI-E-EUO-aih-n-03-0-UI 5', mRNA sequence.
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       Normalization and subtraction:
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                       Lennon, G. and Soares, M.B.
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                                                                                                                                                                                                                                                                                                TGCGCACAACATGGACAACTTGGAGAAGCAGCTCATTTGCCCCCATCTGCCTGGAGATGTT 296
                                                                                                                                                                                                                                                                                                                                                                                                                        GCAGGCTCCAGAGCGCCGCGGGATGAACTTCACGGTGGGTTTCAAGCCGCTGCTAGGGGA 236
                                                                                     CGTCTTCCAGGCCTCTAATCCTCTGTGGCAATCCCGGGGCTCCACAACGGTGTCTTCAGG 416
  AGGACGTTTCCGATGCCCATCTTGTAGGCACGAGGTTGTCCTGGACAGGCATGGTGTCTA 476
                                                    CGTCTTCCAGGCCTCGAATCCTCTATGGCAGTCNCGGNGCTCCACCACTGTGTCTTCAGG
                                                                                                                                                               CTCCAAACCAGTGGTGATCCTGCCCTGCCAACAACCTGTGCCGCAAATGTGCCAACGA
                                                                                                                                                                                                                                                               TGCACACAGCATGGACAACCTGGAGAAGCAGCTCATCTGCCCCATCTGCCCTGGAGATGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  405;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: msoares@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genome Res. 6 (9), 791-806 (1996) 97044477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seq primer: M13 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genetics (www.resgen.com).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clone Distribution: Researchers may obtain clones from Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        //dev_stage="fetal and adult"
//dev_stage="fetal and adult"
//lab_host="DH10B (Life Technologies) (Tl phage resistant)"
//note="Organ: eye; Vector: pT773-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-E-EJO is a subtracted cDNA library constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pT773-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)1B tail. The
sequence tags for this library are: fetal eyes, AGAATCAAGA;
lens, CGATTAAGTG; retina, CGCG; Retina FOveal and
Macular, GTCC; RPE and Choroid, ACCTA. This library was
created for the program, Gene Discovery in the Visual
System, supported by National Eye Institute (NEI)."
196 g 116 t 3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tissue_type="fetal eyes, lens, eye anterior segment, ontic nerve, retina, Retina Foveal and Macular, RPE and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            optic nerve, retina,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="UI-E-EJ0-aih-n-03-0-UI"
/clone_lib="UI-E-EJ0"
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86.2%;
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Pred. No. 3.5e-65;
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RESULT 15
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Best Local Similarity
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                                                                                                                                                                                                                                                                  226 CTGCTAGGGGATGCGCACAACATGGACAACTTGGAGAAGCAGCTCATTTGCCCCCATCTGC 285
                                                   346 TGTGCCAACGACGTCTTCCAGGCCTCTAATCCTCTGTGGCAATCCCGGGGCTCCACAACG 405
                                                                                                                                                              286 CTGGAGATGTTCTCCAAGCCCGTGGTGATCTTGCCCTGCCAACACAACCTGTGCCGCAAG
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TGTGCCAATGACATCTTCCAGGCTGCAAATCCCTACTGGACCAGCCGGGGCAGCTCAGTG
                                                                                                        CTGGAGATGTTTACCAAGCCAGTGGTCATCTTGCCGTGCCAGCACAACCTGTGCCGGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://imagge.llnl.gov plate: LLAM11494 row: k column: 01 High quality sequence stop: 793.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
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/clone_lib="NIH_MGC_114"
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                                                                                                                                                                                                                                                                                                                                                    Score 342.6; DB 1
Pred. No. 1.6e-64;
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RESULT 16
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                                                                                                                                                                                                                                                                                                                  Unpublished (1998)
Contact: Lee, NH
Contact: Lee, NH
The Institute for Genomic Research
9712, Medical Center Drive, Rockvi;
Tel: (301)-838-3529
Fax: (301)-838-0208
                                                                                                                                                                                                                                                           This clone is available through the ATCC, tel#703-365-2700 for further information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AW918753 378 bp mRNA linear ES EST350057 Rat gene index, normalized rat, norvegicus, Rattus norvegicus cDNA clone RGIEX57 5' end, mRNA sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lee, N.H., Glodek, A., Chandra, I., Mason, T.M., Kerlavage, A.R. and Adams, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                          primer: M13 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genome Project:
                                                                                                                                                                                                                                                                                               nhlee@tigr.org
                                      liver, embryo, heart, muscle, spleen"
/lab_host="SOLR"
                                                                                                      Bento Soares"
/note="Vector: pBlueScript SK(-); Site_1:
xhol; Estimated insert size approx.1 kb"
                                                                         /tissue_type="mix - brain, ovary, placenta,
                                                                                                              /clone_lib="Rat gene index, normalized rat, norvegicus,
                                                                                                                                          /db_xref="taxon:10116"
/clone="RGIEX57"
                                                                                                                                                                               /organism="Rattus norvegicus"
                                                                                                                                                                                                                    Location/Qualifiers
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                                                                       kidney, lung,
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: msoarss@blue.weeg.uiowa.edu

The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the Notl site and the oligo-dT track served to verify it as a clone from the normalized rat heart pool library cDNA Library Preparation: M.B. normalized rat heart pool library cDNA Library Preparation:
                                                                                                                                                       451 Eckstein Medical Research Building Towa City, Tel: 319 335 8250 Fax: 319 335 9565
POLYA=Yes
                                   Soares Lab Clone distribution: clones will be available through
                                                                                                                                                                                                         Program for Rat Gene Discovery and Mapping University of Iowa
                                                                                                                                                                                                                                     Contact: Soares, MB
                                                                                                                                                                                                                                                       97044477
                                                                                                                                                                                                                                                                  Genome Res. 6 (9), 791-806 (1996)
                                                                                                                                                                                                                                                                                discovery
                                                                                                                                                                                                                                                                                                                Bonaldo, M.F.,
                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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BG375657.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                       BG375657 440 bp mRNA linear EUI-R-CSO-btd-h-03-0-UI.Sl UI-R-CSO Rattus norvegicus UI-R-CSO-btd-h-03-0-UI 3', mRNA sequence.
                       Research Genetics (www.resgen.com)
                                                                                                                                                                                                                                                                                              Normalization and subtraction: two approaches
                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus
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          primer: M13 Forward
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                                                                                                                                                                   DEFINITION
                                                                                                                                                                                                          BG379943/c
                                                               SOURCE
                                                                                KEYWORDS
                                                                                                    VERSION
                                                                                                                                                                                                                                RESULT 18
                                           ORGANISM
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                                                                                                                                                                                                                                                                                                                 ACTCAAGTGTCCC 1431
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                                                                                                                                                                                                                                                                                             ACTCATGTGTCCC 19
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                                                                                                    UI-R-CS0-bto-b-01-0-UI.S1 UI-R-CS0 Rattus norvegicus UI-R-CS0-bto-b-01-0-UI 3', mRNA sequence. BG379943 BG379943.1 GI:13304415
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Rattus norvegicus
                                                                                  EST.
                                                                                                                                                                                       BG379943
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /lab_host="DHIOB (Life Technologies)"
/lab_host="DHIOB (Life Technologies)"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-CS0
library is a normalized library constructed from the
following rat heart tissues: embryonic day 17, embryonic
day 19, embryonic day 21, adult day 1, adult day 12, adult
day 75, adult day 200. For a detailed description of the
library from which this clone was derived, please visit
our web site at ratest.eng.uiowa.edu. The subtraction has
been previously described in (Bonaldo, Lennon and Soares,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAG_TISSUE=rat heart pool TAG_SEQ=ATAAGATAAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="UI-R-CS0"
/dev_stage="ADULT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-CSO-btd_h-03-0-UI"
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Pred. No. 2.2e-64;
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1363 AGACCACCGCGCCACCAAGCTCGGCTTCCCGGCCCCCGGGAAGGTTCTCAATAAAGGACTC 1422
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                                                                                                                                                                                         201 AACACAGGGCTGGAGGAGGAGGCTGGACGGGCCAGAAGGTT-----TGCACTGATCC 148
                                                                                                                                                                                                                                                                                                                 CAGCCGGGCGCCCCTGGGGATGAAGAGGATGACGACATGGCTTTGGATGGGGAGGAGGGC
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                                                               GACTCTGATCCAGAGCGCACGCC-----CGGGAGCCAAGGGATGCTGAGGATCTGCGCAG
                                                                                                                       GACTCTGATCCAGAGCGCACACCCGAAGCGGGAGCCAAGGGATGCTGAGGATCTGCGCAG 1362
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The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution:
clones will be available through Research Genetics (www.resgen.com)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                451 Eckstein Medical Research Building Towa City,
Tel: 319 335 8250
Fax: 319 335 9565
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Bonaldo, M.F., Lennor
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/note-"Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-CSO library is a normalized library constructed from the following rat heart tissues: embryonic day 17, embryonic day 19, embryonic day 21, adult day 1, adult day 12, adult day 12, adult day 12, adult day 17, adult day 12, adult day 18, embryonic day 21 advised description of the library from which this clone was derived, please visit our web site at ratest.eng.uiowa.edu. The subtraction has been previously described in (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)
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/db_xref="taxon:10116"
/clone="UI-R-CS0-bto-b-01-0-UI"
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90.7%;
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406 GTGTCTTCAGGAGGACGTTTCCGATGCCCATCTTGTAGGCACGAGGTTGTCCTGGACAGG
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                                                                                                                                        CTGGAGATGTTCTCCAAGCCCGTGGTGATCTTGCCCTGCCAACACAACCTGTGCCGCAAG 345
                                                                           TGTGCCAACGACGTCTTCCAGGCCTCTAATCCTCTGTGGCAATCCCGGGGCTCCACAACG
                                                                                                                                                                                                     CTGATCCAGGATGGGAATCCCATGGAGAACTTGGAGAAGCAGCTGATCTGCCCTATCTGC
                                                                                                                                                                                                                                      CTGCTAGGGGATGCGCACAACATGGACAACTTGGAGAAGCAGCTCATTTGCCCCCATCTGC 285
                                     TGTGCCAATGACATCTTCCAGGCTGCAAATCCCTACTGGACCAGCCGGGGCAGCTCAGTG
                                                                                                                     CTGGAGATGTTTACCAAGCCAGTGGTCATCTTGCCGTGCCAGCACAACCTGTGCCGGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://image.llnl.gov
Plate: LLCM1722 row: j column: 18
High quality sequence stop: 863.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC http://mgc.nci.nih.gov/
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602737069F1 NIH_MGC_49 Homo sapiens
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Clone distribution: MGC clone distribution information can be
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/clone_lib="NIH_MGC_49"
/clone_lib="NIH_MGC_49"
/tissue_type="melanotic melanoma, high MDR (cell line)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skih; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; CDNA made by oligo-dT priming. Directionally cloned into ECORI/KhoI sites using the following 5' adaptor:
GGCACCAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library. |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         378 CACGGAGTGTACGGCCTGCAGAGGAACCTGCTGGTGGAGAACATCATCGACATCTACAAA 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   466 CATGGTGTCTATGGCCTGCAGCGGAACCTGCTAGTGGAGAACATCATTGACATCTACAAG 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         526 CAGGAGTCCTCCCGGCCACTGCACGCCAAGGCTGAACAGCACCTCATGTGTGAGGAGCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGCGAACTGCTTCAAGCACTGGCCCGGGAGCAGGAGGAGAAGTTGCAGCGCGTGCG-GGG
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                                                                                                                                       Tel: 302-831-1335
Fax: 302-831-2822
                                                                                                                                                                                                      Contact: Larry A. Cogburn
University of Delaware
                                                                                                                                                                                                                                                                                1 (bases 1 to 495)
Cogburn, L.A. and Monsonego-Ornan, E.
ESTs from Normalized Chicken Breast Muscle, Leg Muscle, and
Epiphyseal Growth Plate cDNA library, USDA/IFAFS Animal Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BM488618
495 bp mRNA linear EST 07-FEB-200 pgm2n. pk008.d8 Normalized Chicken Breast Muscle, Leg Muscle, and Epiphyseal Growth Plate cDNA library (pgm2n) Gallus gallus cDNA clone pgm2n.pk008.d8 5' similar to ref[NP_067422.1 (NM_021447) muscle-specific RING-finger protein; 4930486E09Rik [Mus musculus] gb|AAG03076.1| (AF294790) RING-finger protein MURF [Mus musculus],
                                                                                                                                                                                                                                                  Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gallus gallus
                                                                                                                                                                            Townsend Hall, Newark, DE 19717,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence.
8618
                                                                                                             cogburn@udel.edu, www.chickest.udel.edu
/organism="Gallus gallus"
/strain="Commercial broile
Strains 90 & 21"
                                                                                        ocation/Qualifiers
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                       broiler
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                                                                                                                                                                                                                                                                                                                                                                                       296 TCTCCAAGCCCGTGGTGATCTTGCCCTGCCAACACA-ACCTGTGCCGCAAGTGTGCCAAC 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             176 GGCAGGCTCCAGAGCGCCGCGGGATGAACTTCACGGTGGGTTTCAAGCCGCTGCTAGGGG 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               y Match 22.9%; Score 327.8; DB 13; Length 495; Local Similarity 79.3%; Pred. No. 2.2e-61; hes 388; Conservative 0; Mismatches 100; Indels 1; Gaps
                                                                                                                    TACGGGCTGCAGCGGAACCTGCTGGTGGAGAACATCATCGACATCTACAAGCAGGAATCG 365
                                                                                                                                                                                                                                                                                                                     TATGGCCTGCAGCGGAACCTGCTAGTGGAGAACATCATTGACATCTACAAGCAGGAGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GACGTCTTCCAGGCCTCTAATCCTCTGTGGCAATCCCGGGGCTCCACAACGGTGTCTTCA 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATGCGCACAACATGGACAACTTGGAGAAGCAGCTCATTTGCCCCCATCTGCCCTGGAGATGT 295
                                             GGCGCCCAC 663
                                                                                             CGCATCAACATCTACTGCCTGCGCTGCGNNNCGCCCACCTGCTCCCTCTGCAAGGTGTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGAGNNNTACCGGGACCGCGGAGATGAACTTCGCGGTGGGGGCTGAAGCCGCTGCTGGCGG 65
GGCGCTCAC 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: pCMVSPORT6; Library made from equivalent pools of total RNA isolated from each tissue (embryonic muscle 33.3%; juvenile muscle 33.3%; and epiphyseal growth plate 33.3% of the final RNA pool). Single pass sequencing from 5'-end"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="pgm2n.pk008.d8"
/clone_lib="Normalized Chicken Breast Muscle, Leg Muscle, and Epiphyseal Growth Plate cDNA library (pgm2n)"
/sex="Male and Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            growth plate"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /dev_stage="Breast,leg:Embryo(d19);post-hatch(1d,1,3,5,7,9
,11 weeks);growth plate(1d,7d,14d post-hatch)"
/lab_host="E. coli EMDH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="Breast muscle, leg muscle and epiphyseal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:9031"
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                                                           US-09-908-988B-1
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1 aaggagtgtagacagagtgt.....ataaaggactcaagtgtccc 1431
                                                                                                                                                        December 3, 2002, 09:13:42; Search time 59 Seconds (without alignments) 7438.211 Million cell updates/sec
                                                                                                                                                                                                                                                                                                     GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
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Minimum DB seq length: 0
Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

441362 segs, 153338381 residues

Word size : Searched:

Post-processing: Listing first 45 summaries

Database : Issued Patents NA:*

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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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N	17		102	-	-08-047-041A-1	ce 15, App
ω	17	1.2	133	۳	-08-047-041A-	e 2, Appl
4	17	1.2	133	N	-08-795-006A-	e 22, App
υ	17	:	133	4	-09-184-073-2	22,
o	17		320	w	-09-	116,
7	17		716	4	-08-998-416-	1129, A
œ ·	17		732	4	-08-998-416-	e 927, Ap
9	17	1.2	800	Н	-08-472-2	1, Appl
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12	17	1.2	1215	L	7-2	Sequence 20, Appl
13	17	1.2	1215	4	'n	e 26,
14	17	1.2	1215	4	ည်	26,
15	17	1.2	1215	4		`
16	17	1.2	1215	G	535	20,
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26	17	1.2	1317	4	-09-305-914-	1,
27	17	1.2	1317	4	-09-685-	۲,

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US-09-385-028-15 US-08-094-071-1	US-09-480-718-45	US-09-170-159A-4	us-09-073-567-12	US-08-801-718-4	US-08-390-515A-4	US-08-390-517A-4	US-08-390-516C-4	US-08-557-393-4	US-08-390-479A-4	US-08-390-546-4	US-08-245-500A-4	US-08-283-911-3	US-08-044-619A-3	US-07-903-103-3	US-07-945-283-3	PCT-US95-15353-1
Sequence 1, Appli	45,		Sequence 12, Appl	4.	Sequence 4, Appli	Sequence 3, Appli	Sequence 3, Appli	Sequence 3, Appli	Sequence 3, Appri	Ļ						

ALIGNMENTS

Query Match Best Local Similarity Matches 17; Conser	APPLICATION NUMBER: US FILING DATE: 17-DEC-19 ATTORNEY/ACENT INFORMATIO NAME: Vincent, Matthew REGISTRATION NUMBER: 3 REFERENCE/DOCKET NUMBER: 100: TELEFAX: 617-832-7000 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 39 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: other nuc DESCRIPTION: /desc = " US-08-767-942A-36	APPLICANT: Guillaume, Co TITLE OF INVENTION: UBIQ NUMBER OF SEQUENCES: 45 CORRESPONDENCE ADDRESS: ADDRESSE: FOLEY, HOAG STREET: One Post Offic CITY: Boston STATE: MA COUNTRY: USA LIP: 02.109-2170 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy di COMPUTER: IBM PC COMPA OPERATING SYSTEM: PC-D SOFTWARE: Patentin Rel	RESULT 1 US-08-767-942A-36 US-08-767-942A-36 ; Sequence 36, Applicat ; Patent No. 6068982 ; Patent No. 6068982 ; Patent No. ROIFONATION: APPLICANT: Chiu, APPLICANT: Berlin ; APPLICANT: Damagn ; APPLICANT: Draett
1.2%; Sco 100.0%; Pr vative 0;	APPLICATION NUMBER: US/08/767,942A FILING DATE: 17-DEC-1996 TORNEY/AGENT INFORMATION: NAME: Vincent, Matthew P. REGISTRATION NUMBER: 36,709 REBERENCE/DOCKET NUMBER: 36,709 REDERATION INFORMATION: TELEPHONE: 617-832-1000 TELEFAX: 617-832-1000 TELEFAX: 617-832-7000 RMATION FOR SEQ ID NO: 36: QUENCE CHARACTERISTICS: LENGTH: 39 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear	me, Cottarel me, Cottarel uBIQUITIN CON u45 2SS: SSS: HOAG & ELIOT Office Square Office Square Office Square Office Square Office Square	SULT 1 -08-767-942A-36 Sequence 36, Application US/08767942A Sequence 16.68982 GENERAL INFORMATION: APPLICANT: Rolfe, Mark APPLICANT: Chiu, M. Isabel APPLICANT: Berlin, Vivian APPLICANT: Damagnez, Veronique APPLICANT: Damagnez, Giulio
core 17; DB 3; Length 39; Pred. No. 87; Mismatches 0; Indels		LLP LLP , version #1.30	

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US-08-047-041A-15
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 01 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 07/330,566
FILING DATE: 29-MAR-1989
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US 07/928,661
FILING DATE: 17-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                        AUTHORS:
JOURNAL:
VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
   y match 1.2%; Score 17; DB 1; Length 102; Local Similarity 100.0%; Pred. No. 85; hes 17; Conservative 0; Mismatches 0; Indels
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                                                                                        ISSUE: 5
PAGES: 1379-1385
DATE: 1986
                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                         CHROMOSOME/SEGMENT: exon
                                                                                                                                                                                                                                               ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 06-DEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/047,041A
FILING DATE: 22-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Banner & Allegretti, Ltd STREET: 1001 G Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15, Application US/08047041A
o. 5527676
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                                                                                                                                                                                                                                                                                                                                                                           102 base pairs
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                                                                                                                                                          Mol. Cell. Biol
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Fearon, Eric R.
Nigro, Janice M.
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                                                                                                                                                                                                                                         Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US 07/446,584
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Gaps
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US-08-047-041A-2
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 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08047041A Patent No. 5527676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION UMBER: US 07/928,661
FILING DATE: 17-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 06-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 07/330,566
FILING DATE: 29-MAR-1989
ATTORNEY/AGENT INFORMATION:
NAME: KEGEN SETED.
                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                              PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
                                                                                                                                                                                                                POSITION IN GENOME:
                                                                                                                                                                                                                                                  MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 22-MAR-199
                                                    JOURNAL: Gene
VOLUME: 70
PAGES: 245-252
DATE: 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1007 CCATGGAGGAGCCGCAG 1023
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Fearon, Eric R. APPLICANT: Nigro, Janice M. TITLE OF INVENTION: DetectiTITLE OF INVENTION: Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                                                                                  TITLE: A variation in the structure of the TITLE: protein-coding region of the human p53 gene
                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 202-508-9299
                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: doub
TOPOLOGY: linear
                                                                                                                                                               AUTHORS:
                                                                                                                                                                                                                                      ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Kagan, Sarah A. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                   CHROMOSOME/SEGMENT:
                                                                                                                                                                                                                                                                                                                                        LENGTH:
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CITY: Washington
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1001 G Street, N.W.
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                                                                                                                                                                                                                                                                                     linear
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1.2%;
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Best Local Similarity

100.0%;

Score 17; Pred. No.

DB 1; Length 133; 85;

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RESULT 4
US-08-795-006A-22
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                                                                                                             Sequence 22, Application US/09184073 Patent No. 6183964 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY AGENT INFORMATION:
NAME: Kagan, Sarah A
REGISTRATION NUMBER: 32141
REFERENCE/DOCKET NUMBER: 0110
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Boeke, Jef
APPLICANT: Brachmann, Rainer
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING P53
TITLE OF INVENTION: MUTATIONS WHICH SUPPRESS P53 CANCER MUTA- TIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
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SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
             APPLICANT: Boeke, Jef
APPLICANT: Brachmann, Rainer
APPLICANT: Brachmann, Rainer
TITLE OF INVENTION: MUTATIONS WHICH SUPPRESS P53 CANCER MUTA- TIONS
NUMBER OF SEQUENCES: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 133 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                   1007 CCATGGAGGAGCCGCAG 1023
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/795,006A FILING DATE: 05-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                    42 CCATGGAGGAGCCGCAG 58
                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
   ADDRESSEE:
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1001 G Street, NW
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ilarity 100.0%;
Conservative (
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Banner & Witcoff
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Pred. No.
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                                                                                                                                                                                                                                                                                                                      DB 2;
. 85;
                                                                                                                                                                                                                                                                                                      0;
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                                                                                                                                                                                                                                                                                                      0,
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US-09-184-073-22
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                Query Match
Best Local Similarity
Thes 17; Conserve
                                                                                                     ; ORGANISM: Homo sapiens US-09-157-177-116
                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 116, Application US/09157177 Patent No. 6090558
                                                                                                                                                    SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 116
LENGTH: 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                             APPLICANT: MONFORTE, JOSEPH A.
APPLICANT: Becker, Christopher H.
APPLICANT: Becker, Christopher H.
TITLE OF INVENTION: DNA TYPING BY MASS SPECTROMETRY WITH POLYMORPHIC DNA
TITLE OF INVENTION: REPEAT MARKERS
TILE REFERENCE: GSTR:017/GETR017P
CURRENT APPLICATION NUMBER: US/09/157,177
CURRENT FILING DATE: 1998-09-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Butler, John M. APPLICANT: Li, Jia
                                                                                                                                                                                                       EARLIER APPLICATION NUMBER: 60/059,415
EARLIER FILING DATE: 1997-09-19
NUMBER OF SEQ ID NOS: 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
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                                                                                                                                        TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
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CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42 CCATGGAGGAGCCGCAG 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM:
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27 ATAGACAGGGGTGAGAG 43
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17; Conserv
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                                                 1.2%; Score 17; DB 3; 100.0%; Pred. No. 83;
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237 ATAGACAGGGGTGAGAG 253

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US-08-998-416-927
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RITING DATE: 31-DEC-122.

ATTORNEY/AGENT INFORMATION:

NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976

TELECOMMUNICATION INFORMATION:

"PPT.EPHONE: 919-541-8689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-998-416-1129
                                                                         Sequence 927, Application US/08998416 Patent No. 6239264 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                Query Match
Best Local
                                 GENERAL INFORM
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1129, Application US/08998416 Patent No. 6239264
                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 1129:
SEQUENCE CHARACTERISTICS:
LENGTH: 716 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                1192 GCCGCTGGGGATGAAGA 1208
                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
ORIGINAL SOURCE:
      APPLICANT:
                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: GENOMIC DNA SEQU
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                                                                                                                                                                                                                                                            Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY:
STATE:
                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/0 FILING DATE: 24-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                             ORGANISM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSEE: No. 6239264artis Corporation
T: 3054 Cornwallis Road
Research Triangle Park
: No. 6239264th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                              716 base pairs
               Pohlmann, Rainer
Steiner, Sabine
Mohr, Christine
Wendland, Jurgen
                                                                                                                                                                                                                                                Conservative
                                                            Philippsen,
                                                                                                                                                                                                                                                                                                                          PAG1688RP
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REDUENCES OF ASHBYA GOSSYPII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wendland, Jurgen
Knechtle, Philipp
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Steiner, Sabine
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                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                     DNA (genomic)
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                                               Rainer
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                                                              Peter
                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                            Score 17; DB 4; Length 716; Pred. No. 82;
                                                                                                                                                                                                                                               Mismatches
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RESULT 9
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                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08472239 Patent No. 5728526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 919-541-858
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:

APPLICATION NUMBER: CH 0016/97

FILING DATE: 31-DEC-1996

ATTORNEY/ACENT INFORMATION:

NAME: Meigs, J. Timothy

REGISTRATION NUMBER: 38,241

REGISTRATION NUMBER: 38,241
                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                               TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                APPLICANT: GEORGE, Jr., Albert | APPLICANT: BHATNAGAR, Satish K. APPLICANT: NAZARENKO, Irena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1192 GCCGCTGGGGATGAAGA 1208
                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                   526 GCCGCTGGGGATGAAGA 542
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TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
                                                                                                     STREET: P.O. Box
CITY: Alexandria
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS: ADDRESSE: No. 6239264artis Corporation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Knechtle, Philipp
                    MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compati
                                                                         COUNTRY: United States ZIP: 22313-1404
   OPERATING SYSTEM:
                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 24-DEC
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Research Triangle Park
No. 6239264th Carolina
                                                                                                                                              E: BURNS, DOANE, SWECKER & MATHIS P.O. Box 1404
                                                                                                                                                                                                                                                                                    GEORGE, Jr., Albert L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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24-DEC-1997
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                                                                                                                                                                                                                  SEQUENCE AND KIT THEREFOR
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                                                                                                                                                                                                                                 METHOD FOR ANALYZING A NUCLEOTIDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 17; pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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. 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 732;
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RESULT 10
US-09-414-436-4
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                                                                                                                                                                                                  RESULT 11
US-08-347-792-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 4
                                            PATENT NO. JOING PATENT NO. B. APPLICANT: Halazonetis, Thanos D. APPLICANT: Halazonetis, Thanos D. TITLE OF INVENTION: p53 Proteins With Altered TITLE OF INVENTION: Tetramerization Domains TITLE OF INVENTION: 37
                                                                                                                                                            Sequence 20, Application US/08347792 Patent No. 5573925
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Compositions and Methods Based Upon an Isoform of p53 FILE REFERENCE: p53f CURRENT APPLICATION NUMBER: US/09/414,436 CURRENT FILING DATE: 1999-10-07 EARLIER APPLICATION NUMBER: 60/103,849 EARLIER FILING DATE: 1999-10-09 NUMBER OF SEQ ID NOS: 5
                                                                                                                                                                                                                                                                                                                                                                                    Best
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APPLICANT: Mann, Michael J.
APPLICANT: Dzau, Victor J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (703) 836-2021 INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1070
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Mukai, Robert G.
REGISTRATION NUMBER: 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
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LENGTH: 800 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1007 CCATGGAGGAGCCGCAG 1023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                         1007 CCATGGAGGAGCCGCAG 1023
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr., PO Box 457
                                                                                                                                                                                                                                                                                 115 CCATGGAGGAGCCGCAG 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/472,239
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                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                       1.2%; Score 17; DB 4; Length 1070; illarity 100.0%; Pred. No. 81; Conservative 0; Mismatchen
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 Mismatches

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; MOLECULE TYPE: US-08-347-792-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence 20, Ap
sequence 20, Ap
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INFORMATION FOR SEQ ID NO: 20
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE 1215 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 28-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1007 CCATGGAGGAGCCGCAG 1023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 215-540-9206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Halazonetis, Thanos D.
TITLE OF INVENTION: p53 Proteins With Altered
TITLE OF INVENTION: Tetramerization Domains
                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
              TELECOMMUNICATION INFORMATION: TELEPHONE: 215-540-9206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/347,792 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 19477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Spring House
STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
TOPOLOGY: lir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Bak, Mary E. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM:
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                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                  STATE:
                                                                                                                                                                                                                                                                                                                                                                                  CITY: Spring House
                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                               19477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/08431357
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SYSTEM: PC-DOS/MS-DOS
215-540-5818
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                                                                                                                    UMBER: US 08/347,792
28-NOV-1994
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100.0%; Pred. No.
tive 0; Mismatc
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Gaps

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INFORMATION FOR SEQ ID NO:

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                                                                Query Match
Best Local Similarity 100.0%; p
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                     NAME: POSOTSKE, Laurence H.
REGISTRATION NUMBER: 34,698
REFERENCE/DOCKET NUMBER: 0486
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 508-9100
TELEFAX: 202 508-929
                                                                                                                                                                                                                                                                                                        TELEFAX: 202 508-9299
INFORMATION FOR SEQ ID NO: 26:
                              1007 CCATGGAGGAGCCGCAG 1023
                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 1215 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                             MOLECULE TYPE:
ORIGINAL SOURCE:
ORGANISM: Hom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Halazonetis, Thanos APPLICANT: Hartwig, Wolfgang TITLE OF INVENTION: Peptides no TITLE OF INVENTION: Structural TITLE OF INVENTION: Function NUMBER OF SEQUENCES: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1007 CCATGGAGGAGCCGCAG 1023
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26 CCATGGAGGAGCCGCAG 42
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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STREET: LUCE
STREET: LUCE
STREET: LUCE
Washington,
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STRANDEDNESS: double
TOPOLOGY: linear
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                                                                                                                                                             Homo sapiens
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                                                                                 1.2%; Score 17; DB 4; Length 1215; L00.0%; Pred. No. 81;
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                                                                    Mismatches
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RESULT 14

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GENERAL INFORMATION:
APPLICANT: Halazonetis, Thanos
APPLICANT: Hartwig, Wolfgang
ITILE OF INVENTION: Peptides and peptidomimetics with
TITLE OF INVENTION: Peptides and peptidomimetics with
TITLE OF INVENTION: Structural similarity to human p53 that activate p53
TITLE OF INVENTION: function
FILE REFERENCE: 2973.19998
CURRENT APPLICATION NUMBER: US/08/894,327
CURRENT FILING DATE: 1997-12-04
EARLIER APPLICATION NUMBER: pctus96/01535
EARLIER FILING DATE: 1996-02-16
EARLIER FILING DATE: 1995-02-16
EARLIER FILING DATE: 1995-02-16
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 3.0
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LENGTH: 1215
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Best Local S
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                                                TELEFAX: 202 508-9299 INFORMATION FOR SEQ ID NO: 26:
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MEDIUM TYPE: Floppy disk

COMPUTER: IEM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                             APPLICATION NUMBER: 08/392,542
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
SEQUENCE CHARACTERISTICS:
LENGTH: 1215 base pairs
                                                                                                                 NAME: POSOTSKE, Laurence H.
REGISTRATION NUMBER: 34,698
REFERENCE/DOCKET NUMBER: 0486.48439
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/685,027
FILING DATE: 10-Oct-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
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TITLE OF INVENTION: Peptides nad Peptidomimetics with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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17; Conserv
                                                                                           TELEPHONE: 202 508-9100
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STREET: 1001 G Street, N.W.
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100.0%; Pred. No. 81;
tive 0; Mismatches
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US-09-685-027-26
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                                                                     ; TOPOLOGY: 1:
; MOLECULE TYPE:
PCT-US95-15353-20
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                Query Match
Best Local Similarity
                                                                                                                                                                                            TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 20:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: The Wistar Institute of Anatomy
APPLICANT: and Biology
APPLICANT: Halazonetis, Thanos D.
TITLE OF INVENTION: p53 Proteins With Altered
TITLE OF INVENTION: Tetramerization Domains
                                                                                                                                                                                                                         REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WST58CPCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9206
                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 1215 base pair:
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                                                                                                                                                                                                                                                                                                             FILING DATE: 01-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 28-APR-1995 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US OF THE THE DATE: 28-NOV-1994
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                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/456,623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: cDNA ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens SEQUENCE DESCRIPTION: SEQ ID NO: 26:
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17; . Conservative
                                                                                                                    nucleic acid
DEDNESS: double
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STRANDEDNESS: double
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                                                                                                        linear
                                                                                       DNA (genomic)
                    100.0%;
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                1.2%; Score 17;
100.0%; Pred. No.
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   Mismatches
                     DB 5;
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                                    Length 1215;
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US-08-047-041A-13
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1007 CCATGGAGGAGCCGCAG 1023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 07/928,661 FILING DATE: 17-AUG-1992 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Detection of Loss of the Wild-Type p53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 1303 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 202-508-9100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 29-MAR-1989 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 0 FILING DATE: 06-DEC-1989 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                           HYPOTHETICAL:
ANTI-SENSE: I
                                                                                                                                                              PUBLICATION INFORMATION:
                                                                                                                                                                                             POSITION IN GENOME:
                                                                                                                                                                                                                             ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 202 - 19299
TELEPHONE: 202-508-9299
TELEPHONE: 202-508-9299
TELEPHONE: 202-508-9299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Washington
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                                                                                                                             AUTHORS:
JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER:
                                                                                                                                                                                                                                                                                               STRANDEDNESS: double TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                             PAGES: 4650
DATE: 1986
                                                                                                               VOLUME:
                                                                                                                                                                               MAP POSITION:
                                                                                                                                                                                                                ORGANISM:
                                                                                              ISSUE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3, Application US/08047041A 5527676
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                                                                               4650-4656
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Nigro, Janice M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vogelstein, Bert
Baker, Suzanne J.
                                                                                                                                              Harris, N.
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                                                                                                                               Mol. Cell. Biol
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                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                            Homo sapiens
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1.2%;
100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          32,141
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Score 17;
Pred. No.
   DB 1;
81;
                 Length 1303;
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US-08-047-041A-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 202-500 12:
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
1-ENGTH: 1307 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/446,584
FILING DATE: 06-DEC-1989
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                       MAP POSITION: 17p13.1
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                              POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                  ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
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APPLICATION NUMBER: US 07/928,661
FILING DATE: 17-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Baker, Suzanne J.
APPLICANT: Fearon, Eric R.
APPLICANT: Nigro, Janice M.
TITLE OF INVENTION: Detection
TITLE OF INVENTION: Gene
                                                                                                                                                                                                                                                                                                                                                                ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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TITLE: Molecular basis for heterogeneity of the
TITLE: human p53 protein
JOURNAL: Mol. Cell. Biol.
                                                                                                                                                                                                  AUTHORS:
                                                                                                                                                                                                                                                     MAP POSITION:
                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: doub
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01
                                                                                                  VOLUME:
                                                                                                                                                                                                                                                                                                            ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/047,041A FILING DATE: 22-MAR-1993
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5. 5527676
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                     1986
                                           4650-4656
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01107.42917
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                                                                                                                                                                                                                                     RESULT 20
US-08-347-792-1
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Best Local Similarity
"atches 17; Conserva
                                                                                                                                                                                    Sequence 1, Application US/08347792
Patent No. 5573925
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US-07-912-011-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                 GENERAL INFORMATION:
APPLICANT: Halazonetis, Thanos D.
TITLE OF INVENTION: p53 Proteins With Altered
TITLE OF INVENTION: Tetramerization Domains
NUMBER OF SEQUENCES: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No.
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                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                              1007 CCATGGAGGAGCCGCAG 1023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 1317 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Feit, Irving N.
REGISTRATION NUMBER: 28,0
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
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TELEPHONE: 212-645-1405
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CURRENT APPLICATION DATA:
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ADDRESSEE: ImClone Systems Incorporated
STREET: 180 Varick Street
                                                                                                                                                                                                                                                                                                                                          134 CCATGGAGGAGCCGCAG 150
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TITLE OF INVENTION: Probes for Detecting Mutant p53
NUMBER OF SEQUENCES: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity nes 17; Conserv
     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: ZLZ C. TELEPHONE: Z
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COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
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IBM PC compatible
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STREET: Spring House Corporate Cntr., PO Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTYR: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYBE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYBE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYBE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYBE: J1047
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYBE: J1047
CUSTON: J104
COMPUTER READABLE FORM:
MAGE: Bak Mary E.
MATCHENY APPLICATION INTRABER: J17, J25
COMPUTER STRATION.
MAME: Bak Mary E.
MAME: Bak Mary E.
MATCHENY AGENT INFORMATION:
MAME: Bak Mary E.
MATCHENY AGENT INFORMATION:
MAME: Bak Mary E.
MATCHENY AGENT INFORMATION:
MAME: STRAINDENESS: J004
CTELEPHONE: J15-540-5918
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LEEPTAX: J137 base pairs
TYPE: Uncleic acid
STRAIDEDHESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE: CDS
LOCATION: J136..1314
US-08-347-792-1
US-08-348-7-792-1
US-08-348-7-792-1
US-08-348-7-792
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Run on:
                                                                                       OM nucleic - nucleic search, using sw model
                                           December 3, 2002, 09:10:27;
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; Search time 265 Seconds (without alignments) 12160.791 Million cell updates/sec
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Sequence: Title: Perfect score: 1 aaggagtgtagacagagtgt.....ataaaggactcaagtgtccc 1431 US-09-908-988B-1 1431

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

2,185,239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: Word size :

4577

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:

/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:

/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:

/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:

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/SIDSZ/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
/SIDSZ/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
/SIDSZ/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

© ~ ~ [] ~ ~ @	Result
14 4 3 3 3 3 5 5 2 8 5 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	Score
100.0 2.55 2.55 2.55 2.55 2.60	Query Match Length DB
1431 65 1349 1913 1990 2040 2040 1500 1500	Length
24 22 22 22 24 24 24 24	DB
ABA99061 ABA52379 AAA72433 AAH68563 AAH78026 ABA95313 AAF27653 AAC75760 ABA99063	ID
Murine muscle ring Mouse spliced tran Human nucleic acid- Human protein HP03 Human proteide sequenc Human cytoskeleton DNA encoding human Human ORFX ORF1315 Murine muscle ring	Description

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22	24	23	15	23	23	22	22	22	22	22	22	22	22	22	22	23	23	23	23	23	23	24	22	22	22	22	24	24	24	23	23	23	21	22	22
AS392	761	BL002	AQ623	AS729	S704	L044	S304	L044	S304	L044	S304	090	D134	K530	K520	S729	S656	S700	S7598	5729	S7048	K351	F8246	52283	S2258	AB201	N6044	K3452	K6217	L1474	L1474	L2423	AAC09207	S2585	631

Rat cDNA clone P00 Human cDNA encodin

Human cDNA encodin Human cDNA encodin Human wound healin

Human cancer relat Human cDNA for nov Rat sequence diffe

DNA encoding novel

DNA encoding novel

Drosophila melanog

Drosophila melanog

Drosophila melanog Human secreted pro Human cDNA encodin

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ALIGNMENTS

DNA encoding novel Human reproductive DNA encoding novel DNA encoding novel PCR primer Fp53-B

Human silent nonco Human dehydrogenas Novel human diagno

Human reproductive DNA encoding novel

Human reproductive

DNA encoding novel

Human HulfRG-3 pro Human secreted pro Human polynucleoti Human polynucleoti DNA encoding novel DNA encoding novel DNA encoding novel

RESULT 1 ABA99061 ABA99061 standard; DNA; 1431 BP. Muscle ring finger; MURF-1; mouse; cardiant; microtubule; intermediate filament; striated muscle; cardiac hypertrophy; Murine muscle ring finger protein 1 (MURF-1) coding sequence ABA99061; 15-JUL-2002 (first entry)

Location/Qualifiers 199..1299 /*tag= /product= "MURF-1"

Mus musculus.

heart disease; gene; ds.

WO200206318-A2.

24-JAN-2002.

18-JUL-2001; 2001WO-US22896.

18-JUL-2000; 2000US-219020P.

Olson EN, (TEXA) UNIV TEXAS SYSTEM. Spencer JA;

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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel muscle ring finger protein useful for drug screening, and diagnosing and treating diseases, particularly cardiomyopathies
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                                                                        CTGCAGCGGAACCTGCTAGTGGAGAACATCATTGACATCTACAAGCAGGAGTCCTCCCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 0;
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                                    CAGATGGCTCTCTACCTCCAGCAGGCAAAGGAGCTGATCAACAAGGTCGGGGCAATGTCG
                                                                               ACACCCGAAGCGGAGCCAAGGGATGCTGAGGATCTGCGCAGAGACCACCGCGCCACCAA
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WO200210449-A2
                                                               splice variant;
                                                                                      Mouse spliced transcript detection oligonucleotide SEQ ID NO:25127
                                             Mus musculus
                                                                                                             15-JUL-2002
                                                                                                                                 ABN52379;
                                                                                                                                                  ABN52379 standard; DNA; 65 BP
                                                                  mouse; rat; splice transcript; detection; RNA transcript;
                                                                                                            (first entry)
                                                              transcriptome;
                                                           oligonucleotide library; ss
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Wed Dec
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28-JUL-2000; 2000US-221607P. 3 to late
02-MAX-2001; 2001US-287724P. 3
                                                                                                                                                                                                             New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription unit of a genome, useful for detecting tissue-, pathology-, and developmental-specific genes
                                                                                                                                                                                                                                                 WPI; 2002-257383/30
                                                                                                                                                                                                                                                                             (COMP-) COMPUGEN INC
                                                                                                                                                                                             Example 1; SEQ ID 25127; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                       4
                                                                                                                                                                                                                                                               Wasserman A,
                                                                                                                                                                                                                                                                                                                                                       10:56:39 2002
                                                                                                                                                                                                                                                                Mintz E, Mintz L,
                                                                                                                                                                                                                                                                Faigler S;
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The present invention describes oligonucleotide libraries for detecting CC messenger RNAs that populate a (sub-)transcriptome, where the CC (sub-)transcriptom units that populate a genome. The library comprises cCC several oligonucleotides, each capable of hybridising selectively to a CC set of messenger RNAs transcribed from multiple CC the genome, which encodes one or more messenger RNA splice variants. CC the contracterising the corresponding transcriptome, and in CC contitatively characterising the corresponding transcriptome, and in CC transcriptomes. The libraries may also be used as specialised mini CC transcriptomes. The libraries may also be used as specialised mini CC particular biological or pathology-specific genes such as those genes conjugation; to detect transcripts of a sub-transcriptome under a particular biological or pathology-specific genes such as those genes conjugation; to detect developmental specific pathological CC condition; to detect developmental specific penes; and to detect RNA CC condition; to detect developmental specific pathological of conjugations and splice variants of a transcriptome of a particular disorder. ABN27253 to ABN59589 represent conjugation of the present invention.

CC at fire who introduce data for this patent did not form part of the printed contraction, but was obtained in electronic format directly from WIPO at the pathology-whiled and the general contract. ftp.wipo.int/pub/published_pct_sequences.

밁 Query Match Best Local 1174 ATCGA 1178 Sequence 65 BP; 17 A; 13 C; 21 G; 14 T; 0 other; 61 Local Similarity 65; Conservative 100.0%; 4.5%; Mismatches Score 65; pred. No. 1.7e-21; DB 24; 0; Length 65; Indels 0; 0

밁 δÃ AAA72433 19-DEC-2000 AAA72433; AAA72433 standard; cDNA; 1349 BP ATCGA 65 (first entry)

RESULT 4 AAH68563

AAH68563 standard; cDNA; 1913

0;

13-SEP-2001 AAH68563;

(first entry)

Human; gene therapy; tumour; ss Human protein HP03115 coding sequence. Human nucleic acid-binding protein NuABP-52 cDNA.

Human nucleic acid-binding protein; NuABP; agonist; antagonist; EST; expressed sequence tag; drug screening; recombinant expression; antibody; reproductive disorder; infertility; immunological disorder; neurological disorder; cell proliferative disorder; cancer; tumour; ss

> 밁 Matches Query Match Sequences AAA72382-A72436 represent cDNAs encoding novel human nucleic acid-binding proteins (NuABPs; AAB20997-B21051). These cDNAs were produced by extension from an appropriate EST (expressed sequence tag) using primers designed using the EST. The invention also relates to expression constructs, host cells and transgenic organisms comprisin a human NuABP nucleic acid, recombinant production of the human NuABPs, and antibodies against the human NuABPs and also to methods of screening modulators of human NuABPs, and also to methods of the human NuABPs, and their agonists and antagonists are used to treat diseases associated with overexpression or underexpression of functional NuABPs. 28-JAN-2000; 2000MO-USO2237. < traffig houble what ATPA 03-AUG-2000. dookto WO200044900-A2. that may be treated using compositions of the invention include infertility, endometriosis, disruptions of the menstrual cycle and disruptions of spermatogenesis. Immunological disorders that may be treated include AIDS, allergies, and autoimmune disorders such as multiple sclerosis, rheumatoid arrhritts, diabetes and systemic lupus erythematosus. Neurological disorders that may be treated include parkinson's disease, prion diseases such as Creutzfeldt-Jakob disease, and mental disorders such as schizophrenia. Cell proliferative diseases that may be treated include a wide variety of cancers, and also that may be treated include a wide variety of cancers, and also Novel nucleic acid binding proteins, used to identify agonists and antagonists of them, for the treatment of reproductive, immunologic neurological and cell proliferative disorders including cancer -29-JAN-1999; 29-JAN-1999; Homo sapiens Human NuABP proteins and nucleotides, and NuABP agonists and antagonists can be used to diagnose, treat and prevent reproductive, immunological, neurological and cell proliferative disorders. Reproductive disorders Claim 4; Page 178-179; 180pp; English. Tran B, (INCY-) INCYTE PHARM INC. 1029 CGGCCGGAGCCAGGCTATGAGAGCATGGAGCAATTC 1064 1099 CGGCCGGAGCCAGGCTATGAGAGCATGGAGCAATTC 1134 Sequence 1349 BP; 328 A; 372 C; 428 G; 221 T; 0 other; arteriosclerosis, atherosclerosis, cirrhosis and psoriasis Local 2000-499332/44. Similarity Shih LL, Conservative 99US-0117904. 99US-0117905. Hillman JL, Au-Young JL; 2.5%; Score 36; DB 21; 100.0%; Pred. No. 2.6e-07; 0; Yue H, Azimzai Y, Mismatches Length 1349; Lu AMD, immunological, Baughn MR; 0; Gaps

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AAH78026
ID AAH7
XX AAH7
XX 26-N
XX 26-N
XX Huma
KW Huma
KW 1eft
XW vent
XX Vent
XX Vent
XX Vent
XX Vent
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                                                                                                                                                                                                                                                                           RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local :
W0200162767-A1
                                                                                                           Human; cardiomyopathy associated protein; CAP; myocardial biopsy; left ventricle assist device; LVAD; cardiomyopathy; ventricular tachyrhythmia; ss.
                                                                                                                                                            Nucleotide sequence of human cardiomyopathy associated protein (CAP).
                                                                                                                                                                                                                                                                                                            1203 CGGCCGGAGCCAGGCTATGAGAGCATGGAGCAATTC 1238
                                                                                                                                                                                                                                                                                                                                     1099 CGGCCGGAGCCAGGCTATGAGAGCATGGAGCAATTC 1134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-DEC-1999;
06-DEC-1999;
08-FEB-2000;
10-FEB-2000;
                                                                                         Homo sapiens
                                                                                                                                                                                                                         AAH78026;
                                                                                                                                                                                                                                             AAH78026 standard; cDNA; 1990 BP
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1913 BP; 446 A; 537 C; 612 G; 318 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is a human protein coding sequence. The human protein, preferably originated from tumour cell line, is applicable as a drug, a reagent for studying intracellular protein networks and a protein source for screening proteins for binding low molecular weight drugs. The human protein coding sequence is useful for gene diagnosis and gene therapy, expression vectors and transformant cells for detection of
                                                                                                                                                                                              26-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human protein originated from tumor cell line, applicable as drug, reagent for studying intracellular protein networks and protein so for drug screening, also encoded cDNA for gene diagnosis and gene
                                                                                                                                                                                                                                                                                                                                                                                                                                              ligands and receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 3; Pages 236-240; 471pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (NISC-) JAPAN SCI & TECHNOLOGY CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2001-381646/40.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eguchi C,
                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                   Conservative
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99JP-346864.

2000JP-0031062.

2000JP-0034090.

2000JP-0034091.

2000JP-0035829.

2000JP-0071161.

2000JP-0160851.
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                   /product= "cardiomyopathy associated protein (CAP)"
                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                              2.5%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saeki M;
                                                                                                                                                                                                                                                                                                                                                                              Score 36; DB 22; 
; Pred. No. 2.6e-0
                                                                                                                                                                                                                                                                                                                                                                  0;
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                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                             2.6e-07;
                                                                                                                                                                                                                                                                                                                                                                  0,
                                                                                                                                                                                                                                                                                                                                                                                         Length 1913;
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ABN85313
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Best Local (
04-JAN-2002; 2002WO-US00178. OK MIAA MA
                                                                                                                                                                                                                                      Human; cytoskeleton-associated protein; CSAP; CSAP-4; cell proliferative disorder; viral infection; neurological disorder; transgenic animal; antiatherosclerotic; antipsoriatic; antiinflammatory;
                                                                                                                                                                                                                                                                                                      Human cytoskeleton-associated protein, CSAP-4, coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1183 CGGCCGGAGCCAGGCTATGAGAGCATGGAGCAATTC 1218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1099 CGGCCGGAGCCAGGCTATGAGAGCATGGAGCAATTC 1134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein (CAP) that is differentially expressed in human left ventricle assist device (LVAD) myocardial biopsy samples. The predicted isoelectric point of CAP is approximately 12.2. The CAP polynucleotide and polypeptide are useful for diagnosing, preventing or treating cardiomyopathy. The treatment diminishes the occurrence of at least one of the following symptoms associated with cardiomyopathy: reduced ejection fraction, increased left ventricular diagnosing dimension,
                                               11-JUL-2002.
                                                                            WO200253719-A2
                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                            neuroprotective; cytostatic; gene therapy; gene; ss.
                                                                                                                                                                                                                           virucide; anticonvulsant; vasotropic; cerebroprotective; nootropic;
                                                                                                                                                                                                                                                                                                                                                                             ABN85313;
                                                                                                                                                                                                                                                                                                                                                                                                    ABN85313 standard; cDNA; 2040 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1990 BP; 524 A; 535 C; 613 G; 318 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 decreased ventricular wall thickness, increased atrial size, valvular regurgitation, exertional intolerance or ventricular tachyrhythmia. Modulators of CAP are also useful for preventing or treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid encoding a cardiomyopathy associated protein that is differentially expressed in human left ventricle assist device (LVAD) myocardial biopsy samples, useful for diagnosing, preventing or treating cardiomyopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cardiomyopathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence encodes a human cardiomyopathy associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 2; Page 49-51; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; AAG63832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-FEB-2000; 2000US-0184825.OK Son HTM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-FEB-2001; 2001WO-US05888.OK Sar NZM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GENE-) GENE LOGIC INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001-570621/64.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Greene J,
                                                                                                                                     Location/Qualifiers 291..1271
                                                                                                        /product= "CSAP-4"
                                                                                                                        /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               White M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 36; DB 22;
Pred. No. 2.6e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1990;
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PF PR XX PR XX PA XX PA XX
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13-FEB-2001; 2001US-268554P. A to late
14-FEB-2001; 2001US-269111P. A to late
23-FEB-2001; 2001US-271211P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is the coding sequence for a human cytoskeleton-associated protein (CSAP). The CSAP and its coding sequence are useful in the diagnosis, treatment and prevention of a cell proliferative disorder such as actinic keratosis, atherosclerosis, psoriasis, primary thrombocythaemia, leukaemia, a viral infection such as psoriasis, primary thrombocythaemia, leukaemia, a viral infection such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel isolated human cytoskeleton-associated protein for diagnosing, treating or preventing atherosclerosis, psoriasis, leukemia, epileps; ischemic cerebrovascular disease, cerebral neoplasms and Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              those caused by adenoviruses (acute respiratory disease, pneumonia), arenaviruses (lymphocytic choriomeninigitis); and a neurological disorder such as epilepsy, ischaemic cerebrovascular disease, stroke, cerebral neoplasms, Alzheimer's disease, Pick's disease, Huntington's disease or amyotrophic lateral sclerosis. The CSAP coding sequence is also useful for creating knock out or knock in humanised animals or transgenic animals to model human diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gietzen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Warren BA,
Gandhi AR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (INCY-) INCYTE GENOMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 5; Page 154-155; 167pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1095 CGGCCGGAGCCAGGCTATGAGAGCATGGAGCAATTC 1130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1099 CGGCCGGAGCCAGGCTATGAGAGCATGGAGCAATTC 1134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2040 BP; 465 A; 584 C; 650 G; 341 T; 0 other;
                                                                                                                                                                                                                                               Human; transcriptional regulator protein; TXREG; ds.
                                                                                                                                                                                                                                                                                DNA encoding human transcriptional regulator protein
                                                                                                                                                                                                                                                                                                                   30-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                 AAF27653 standard; DNA; 1500 BP
                                                                                                                                                                                 WO200078954-A2.
                                                                                                             15-JUN-2000; 2000MO-US16766. Not apolloke under AIPA
                 Lal P,
                                              (INCY-) INCYTE GENOMICS INC.
                                                                                 18-JUN-1999;
                                                                                                                                              28-DEC-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Baughn MR, Yao MG, Ding L, Honchell CD, Yue H, Tang YT;
A, Duggan BM, Xu Y, Walia NK, Griffin JA, Stewart EA;
R, Khan FA, Thangavelu K, Ison CH, Azimzai Y, Hafalia AJ,
KJ, Lal PG, Sanjanwala MM, Elliott VS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative (
                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                 by leteror local
                                                                                   99US-0140109.
                 Tang YT, Baughn MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 36; ; Pred. No.

 Mismatches

                   Azimzai Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 24;
2.6e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 2040;
                   Tran B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hafalia AJA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated polypeptide with a human transcriptional regulator protein sequence is useful for the diagnosis, prevention and treatment of disorders associated with the immune, reproductive and cardiovascular
                                                                                                                                                                                                                                                                                                                                                 31-MAR-1999;
02-APR-1999;
05-APR-1999;
30-MAR-2000; 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autolimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation; bone damage; cartilage damage; antiinflammatory disease; coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1500 BP; 401 A; 378 C; 439 G; 282 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immunostimulant; thrombolytic; coaqulant; vasotropic; antidiabetic;
hypotensive; dermatological; immunosuppressive; antiinflammatory;
antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human ORFX ORF1315 polynucleotide sequence SEQ ID NO:2629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAC75760 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-MAR-2000; 2000MO-US08621. Not wind bloc and Aft
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200058473-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          thrombosis; contraceptive; ss.
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                                                                                                                                                                                                                                                                                 (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        777 CTGCCCACCATTTACAAACGCCAGAAGAGTGAGCT 811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                        2000US-0540763
                                                                                                                                                                                                                                                                                                                                                                                99US-0127607.
99US-0127636.
99US-0127728.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 22; I
8.1e-07;
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0

Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease.

Shimkets RA, Leach

P-PSDB; AAB41551

2000-602362/57.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local :
Novel muscle ring finger protein useful for drug screening, and
                                                          WPI; 2002-241506/29.
                                                                                   Olson EN, Spencer JA; Haphow
                                                                                                                                                           18-JUL-2000; 2000US-219020P.
                                                                                                                                                                                                                                                                                                                                                                                                           Muscle ring finger; MURF-3; mouse; cardiant; microtubule; intermediate filament; striated muscle; cardiac hypertrophy; heart disease; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Murine muscle ring finger protein 3 (MURF-3) coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activitles such as: cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antibacterial; antivitral; antifungal; antirheumatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an OREX-associated disorder. The
                                                                                                                                                                                              18-JUL-2001; 2001WO-US22896
                                                                                                                                                                                                                                24-JAN-2002.
                                                                                                                                                                                                                                                                  WO200206318-A2.
                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABA99063;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABA99063 standard; DNA; 1597 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    allergies, aplastic anaemia, burns, wounds, bone and cartilage damage nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 650 BP; 171 A; 150 C; 212 G; 116 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 5; Page 1873; 5507pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         211 GTGGGTTTCAAGCCGCTGCTAGGGGATGC 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85 GTGGGTTTCAAGCCGCTGCTAGGGGATGC 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                Location/Qualifiers 299..1330
                                                                                                                                                                                                                                                                                                /product= "MURF-3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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28-JUN-2000; 30-JUN-2000; 07-JUL-2000;

19-MAY-2000; 07-JUN-2000;

2000US-0205515. 2000US-0209467. 2000US-0214886.

18-APR-2000;

17-MAR-2000;

2000US-0189874. 2000US-0190076.

2000US-0198123

07-JUL-2000;

2000US-0216647. 2000US-0216880.

2000US-0215135.

11-JUL-2000;

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RESULT 10
AAS26314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                              hyperproliferative disorder; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; cerebral ischaemia; angiogenesis; nervous system disorder; Alzheimer's disease; infection; ocular disorder; corneal infection; wound healing; epithelial cell proliferation; skin ageing; food additive; preservative; antiproliferative.
                                                                                                                                                                                                                          17-JAN-2001; 2001WO-US01341. TRATIAL ME
31-JAN-2000; 2000US-0179065. but Belluarit is bether
04-FBB-2000; 2000US-01190658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; immunosuppressive; antiarthritic; ss; antirheumatic; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; opthalmalogical; vulnerary; secreted protein; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          stabilisation of striated muscle cells and have cardiant activity. The MURF proteins are useful for screening a candidate substance for MURF protein-binding activity, in a cell, cell-free system or in vivo, and its effect on interaction of MURF with microtubules, homodimerisation of MURF, MURF-1, MURF-2 or MURF-3 stabilisation of microtubules, interaction of MURF with intermediate filaments, e.g. desmin, vimentin and cytokeratin, and heterodimerisation of MURF. The screened compounds are useful for treating and preventing cardiac hypertrophy and heart diseases. MURF proteins are useful as
                                                                                                                                                                                                                      31-JAN-2000;
04-FEB-2000;
                                                                                                                                                                                                                                                                                                        02-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human cDNA encoding a novel secreted protein, Seq ID 493.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAS26314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAS26314 standard; cDNA; 587 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1597 BP; 405 A; 404 C; 438 G; 350 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antigens to immunise animals for the production of antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence encodes murine muscle ring finger protein 3 (MURF-3). The invention relates to a purified muscle ring finger (MURF) protein, selected from MURF-1, MURF-2 and MURF-3. The MURF proteins of the invention are involved in microtubule and intermediate filament
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diagnosing and treating diseases, particularly cardiomyopathies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 4; Page 131-133; 134pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              596 AACATCATTGACATCTACAAGCAGGAGT 623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                505 AACATCATTGACATCTACAAGCAGGAGT 532
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                                                                                                                                                                                                                      2000US-0179065.
2000US-0180628.
                                                                                                                                                                                    2000US-0184664.
2000US-0186350.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 24;
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14-JUL-2000; 26-JUL-2000; 26-JUL-2000; 14-AUG-2000;

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08 - NOV - 2000

17 - NOV - 2000
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01-DEC-2000;
01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
08-DEC-2000;
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17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
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The invention relates to isolated nucleic acid molecules and their encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked include autoimmune diseases e.g. rheumatoid arthitis, hyperproliferative disorders e.g. neoplasms of the breast or liver,
                                                                                                                                                                                                                                      New nucleic acid molecules encoding 461 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions used as food additives or preservatives -
                                                                                                                                                                                                          Claim
                                                                                                                                                                                                                                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                        2001-488783/53.
DB; AAU16327.
                                                                                                                                                                                                        1.
                                                                                                                                                                                                        SEQ ID No 493; 980pp; English.
                                                                                                                                                                                                                                                                                                                                                           Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-0246474
2000US-0246475
2000US-0246476
2000US-0246477
2000US-0246477
2000US-0246523
2000US-0246523
2000US-0246525
2000US-0246525
2000US-0246526
2000US-0246526
2000US-0246528
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2000US-0246610.
2000US-0246611.
                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0249214
2000US-0249215
2000US-0249216
2000US-0249218
2000US-0249245
2000US-0249264
2000US-0249264
2000US-0249264
2000US-0249297
2000US-0249297
2000US-0249297
2000US-0251030
2000US-0251030
2000US-0251030
2000US-02511030
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2000US-0249208.
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2000US-0249210.
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                                                                                                                                                                                                                                                                                                                                                            Ruben SM;
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14-SEP-2000; 14-SEP-2000; 14-SEP-2000;

2000US-0232398 2000US-0232397

2000US-0232399. 2000US-0232400. 2000US-0232401.

14-SEP-2000; 14-SEP-2000; 14-SEP-2000; 14-SEP-2000;

2000US-0234274. 2000US-0234997. 2000US-0234998.

2000US-0234223 2000US-0233063 2000US-0233064

14-SEP-2000;
21-SEP-2000;
25-SEP-2000;
25-SEP-2000;
26-SEP-2000;
27-SEP-2000;
27-SEP-2000;
29-SEP-2000;
21-CCT-2000;
20-CCT-2000;
21-CCT-2000;
21-CC

2000US-0236369 2000US-0236370 2000US-0236802 2000US-0237037

and

2000US-0237038. 2000US-0237039. 2000US-0237040.

2000US-0239935 2000US-0239937 2000US-0240960 2000US-0241221 2000US-0241785 2000US-0241786 2000US-0241787 2000US-0241808 2000US-0241808 2000US-0241809 2000US-0241809 2000US-0241809 2000US-0241809 2000US-0241806

05-SEP-2000 06-SEP-2000 06-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000

2000US-0231242. 2000US-0231243. 2000US-0231244. 2000US-0231413. 2000US-0231414.

2000US-0230437 2000US-0230438 2000US-0229509. 2000US-0229513.

2000US-0232080. 2000US-0232081. 2000US-0231968.

22-AUG-2000; 23-AUG-2000; 30-AUG-2000; 01-SEP-2000; 01-SEP-2000; 01-SEP-2000; 01-SEP-2000; 01-SEP-2000;

14-AUG-2000; 14-AUG-2000; 14-AUG-2000; 14-AUG-2000;

L8-AUG-2000;

2000US-0226868

14-AUG-2000; 14-AUG-2000;

2000US-0218290 2000US-0220963 2000US-0220964 2000US-0224518 2000US-02254519 2000US-0225214 2000US-0225266 2000US-0225267 2000US-0225267 2000US-0225267 2000US-0225267 2000US-0225267 2000US-0225267 2000US-0225270 2000US-0225758

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Best Local
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                                         11-JUL-2000;
14-JUL-2000;
26-JUL-2000;
26-JUL-2000;
14-AUG-2000;
                                                                                                  19-MAY-2000;
07-JUN-2000;
28-JUN-2000;
30-JUN-2000;
07-JUL-2000;
07-JUL-2000;
11-JUL-2000;
        14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
                                                                                                                                                                                                                    31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                 Human; immunosuppressive; antiarthritic; ss; antirheumatic; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; opthalmalogical; vulnerary; secreted protein; rheumatoid arthritis; hyperproliferative disorder; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; cardiac ischaemia; angiogenesis; nervous system disorder; larehmer's disease; infection; ocular disorder; corneal infection; wound healing; epithelial cell proliferation; skin ageing; food additive; preservative; antiproliferative.
                                                                                                                                                                                   17-MAR-2000;
18-APR-2000;
                                                                                                                                                                                                                                                                                                     02-AUG-2001
                                                                                                                                                                                                                                                                                                                            WO200155322-A2
                                                                                                                                                                                                                                                                                                                                                    Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional components. The present sequence encodes a novel secreted protein of the invention.
                                                                                                                                                                                                                                                                             17-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection, and many other disorders listed in the specification. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human cDNA encoding a novel secreted protein, Seq ID 34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAS25855;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAS25855 standard; cDNA; 1762 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                508 ATCATTGACATCTACAAGCAGGAGTCC 534
                                                                                                                                                                                                          -MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                               sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
27; Conserv
                  2000US - 0209467

2000US - 021486

2000US - 0215135

2000US - 0216647

2000US - 0217487

2000US - 0224518

2000US - 0224518

2000US - 0224518
                                                                                                                                                                    2000US-0186350.
2000US-0189874.
2000US-0190076.
2000US-0198123.
2000US-0205515.
                                                                                                                                                                                                                              2000US-0179065.
2000US-0180628.
2000US-0184664.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
       2000US-0225214.
                                                                                                                                                                                                                                                                             2001WO-US01341
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100.0%;
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                                                                                                                                    food additives or preservatives
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                                                                                                                       SEQ ID No 34; 980pp; English.
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New nucleic acid molecules encoding 461 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and

The invention relates to isolated nucleic acid molecules and their encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunoasorbant assays (ELISA). Disorders which are diagnosed or treated Alineimer's disease, infections caused by bacteria, viruses and fur and ocular disorders e.g. corneal infection, and many other disorders listed in the specification. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiovascular disorders e.g. cardiovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. prevent skin aging due to sunburn, maintain

20

211 GTGGGTTTCAAGCCGCTGCTAGGGGA 236

Matches Query Match

Local

Similarity

100.0%;

1.8%; Score 26; 100.0%; Pred. No.

DB 21; Length 341; 0.021;

Conservative

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Mismatches

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Indels

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                                             The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence encodes a novel secreted protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                   diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and fo
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Sequence 341 BP; 114 A; 64 C; 114 G; 49
                                   expression and secretion vectors.
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               Drosophila melanogaster expressed polynucleotide SEQ ID NO 38711
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                                                                                          26-MAR-2002
                                                                                                                                                   ABL14743;
                                                                                                                                                                                                     ABL14743 standard; cDNA; 8574
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genes from Drosophila and
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11-JUL-2000; 2000US-0614150.
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В
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                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
 23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                        23-MAR-2001; 2001WO-US09231
                                                                  27-SEP-2001
                                                                                             WO200171042-A2
                                                                                                                      Drosophila melanogaster.
                                                                                                                                               pharmaceutical; gene; ss.
                                                                                                                                                        Drosophila; developmental biology; cell signalling;
                                                                                                                                                                                   Drosophila melanogaster expressed polynucleotide SEQ ID NO 38708.
                                                                                                                                                                                                                                            ABL14742;
                                                                                                                                                                                                                                                                 ABL14742 standard; cDNA; 13239
                                                                                                                                                                                                                                                                                                                                   3041 AGGAGCGCAAGGGCGAACTG 3060
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8574 BP; 1935 A; 2333 C; 2424 G; 1882 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                 26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 38711; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                            872 AGGAGCGCAAGGGCGAACTG 891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; ABB70640
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Adams M,
2000US-191637P.
2000US-0614150
                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                 1.4°,
100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                                                                            1.4%; Score 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Li PWD,
                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No.
                                                                                                                                                                                                                                                                   BP.
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                                                                                                                                                                                                                                                                                                                                                                                                DB 23; Length 8574;
                                                                                                                                                                                                                                                                                                                                                                                    0;
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                                                                                                                                                                                                                                                                                                                                                                                    0;
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RESULT 16
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABLIG176-ABL30511).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               interactions -
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                                                                                                                                                                                                                                                                                                                               Rat; ss; hepatotoxin; expressed sequence tag; EST; drug screening; differential expression; centrilobular necrosis; steatosis.
                                                                                                                                                                                                                                                                                                                                                                                                     18-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABK62174 standard; cDNA; 488 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7067 AGGAGCGCAAGGGCGAACTG 7048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 13239 BP; 3468 A; 3272 C; 3140 G; 3359 T; 0 other;
                                                                                                                                                   11-MAY-2001;
15-MAY-2001;
                                                                                                                                                                               02-NOV-2000;
                                                                                                                                                                                            31-JUL-2000;
                                                                                                                                                                                                                       30-JUL-2001;
                                                                                                                                                                                                                                                   07-FEB-2002
                                                                                                                                                                                                                                                                           WO200210453-A2
                                                                                                                                                                                                                                                                                                       Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                        Rat sequence differentially expressed in response to a hepatotoxin #81.
                                                                                                                                                                                                                                                                                                                                                                                                                                ABK62174;
                           Mendrick D,
                                                     (GENE-) GENE LOGIC INC
                                                                                                                        06-JUN-2001;
                                                                                                                                        22-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          872 AGGAGCGCAAGGGCGAACTG 891
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 38708; 21pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Adams M,
                                                                                                         2001US-292336P.
2001US-295798P.
2001US-297457P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                      2001WO-US23872
                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                           Porter MW,
                                                                                                                                                   2001US-290029P.
2001US-290645P.
                                                                                                                                                                               2000US-244880P.
                                                                                                                                                                                             2000US-222040P
                                                                               2001US-303459P
                                                                                            2001US-298884P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.4%; Score 20;
100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
                          Johnson KR,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                            Castle AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 23;
17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 13239;
                            Elashoff MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      English.
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CC compounds of the progression of these to take expects by december to global changes in gene expression in tissues or cells exposed to the cells. Also included are methods of predicting at least one toxic ceffect of a compound or progression of a toxic effect, preferably the ceffect of a compound or progression of a toxic effect, preferably the ceptression in a tissue or cell sample exposed to the level of ceptression in a tissue or cell sample exposed to the compound of two or ce expression in a tissue or cell sample exposed to the compound of two or ce expression in a tissue or cell sample exposed to the compound of two or ce expression in a tissue or cell sample exposed to the compound of two or ce expression also be used to identify an agent which modulates the compound can also be used to identify an agent which modulates the compound modulates the cell. The methods utilise a set of at least two probes (on a solid comport in kit form), where each of the probes comprises a sequence that compount modulates to a gene listed in the specification, a computer system comprising at least two genes listed in the specification, a computer comprising at least two genes listed in the specification, a computer set of genes comprising at least two genes listed in the specification, a computer composed to a gene information used to present information composed to a hepatotoxin of a containing information used to present information composed to a hepatotoxin of a containing information used to present information composed in the specification, a composed to a known toxin. The genes may be used as containing the containing global characterised by centrilobular necrosis and steatosis. The present contained the probability markers for the genes and contained toxin in the probability markers for the containing probability and the probability markers for the probability of the containing and steatosis. The present contains the probability of containing and the probability of containing and the probability of containing and t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      predicting toxic effects of compounds or the progression of these effects by determining the changes in gene expression in tissues o cells exposed to the toxin and comparing these to gene expression unexposed tissues or cells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to methods for predicting toxic effects of compounds or the progression of these toxic effects by determining the compounds or the progression in tissues or cells exposed to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Seq ID No 81; 239pp; English
Sequence 488 BP; 93 A; 136 C; 136 G; 123 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 toxic
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Matches Query Match Best Local 1197 TGGGGATGAAGAGGATGAC 1215 19; Similarity Conservative 1.3%; Score 19; 100.0%; Pred. No. 0; Pred. No. Mismatches DB 57; 24; Length 488; 0 Gaps 0;

RESULT 17 ABK34528 ABK34528; ABK34528 standard; cDNA; 596 BP

DЬ QΥ

390 TGGGGATGAAGAGGATGAC

Human cDNA for novel secreted protein, SEQ ID 297

08-MAY-2002

(first entry)

Alzheimer's disease; Parkinson's disease; liver fibrosis; tumour; coagulation disorder; haemophilia; inflammatory disorder; ulcer; Human; ss; gene; secreted protein; immune deficiency; viral infection; bacterial infection; fungal infection; autoimmune disorder; burn; rheumatoid arthritis; multiple sclerosis; autoimmune thyroiditis; diabetes; allergy; asthma; neurodegenerative disease; Crohn's disease; lymphoid cell deficiency. tissue regeneration; wound healing; haematopoiesis; myeloid deficiency;

Homo sapiens

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AC XXX AC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to 625 polynucleotides which have been derived from Ca variety of human tissue sources and which encode novel secreted proteins, their complements and sequences that hybridise to them. CC Also included are a vector comprising the polynucleotide, a host cell CC transformed with the vector, the proteins encoded by the CC polynucleotides, antibodies that bind to the proteins and identification of modulators of the proteins or the expression of the polynucleotide. CC The polynucleotides can be used as probes for the identification and isolation of full length cDNA and genomic DNA. The polynucleotides can be used as nutritional supplements. The protein CC and proteins can also be used as nutritional supplements. The protein CC is useful in the treatment of various immune deficiencies and disorders cutoimmune disorders (e.g. rheumatoid arthritis, multiple sclerosis, CC autoimmune thyroiditis and diabetes) and allergic reactions and CC conditions (e.g. asthma). They are also useful for treating proteins and conditions (e.g. asthma). They are also useful for reactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         neurodegenerative diseases (e.g. Alzheimer's disease, Parkinson's disease), liver fibrosis, coagulation disorders (e.g. haemophilia), inflammatory disorders (e.g. Crohn's disease) and tumours. They are also useful for tissue regeneration, for wound healing and in the treatment of burns, incisions and ulcers. The proteins are also useful for regulating haematopoiesis, for treating myeloid or lymphoid cell deficiencies. The present sequence is one of the 625 cDNA sequences
21-FEB-2002
                                                            WO200214500-A2
                                                                                                                                                                                             gene
                                                                                                                                                                                                                                                                                        Human cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABN60441 standard; cDNA; 629 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1247 CGGGGCTGGAGGAGGAGCG 1265
                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                  Human;
                                                                                                                                                                                                                                                                                                                                                            28-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                            ABN60441;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 596 BP; 116 A; 152 C; 235 G; 93 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Six hundred and twenty five polynucleotides derived from a variety of human tissue sources which encode secreted proteins, useful for treating immune deficiencies and disorders such as autoimmune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 152; 339pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-APR-2000; 2000US-194941P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-MAR-2001; 2001WO-US10295.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    250 CGGGGCTGGAGGAGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                 cytostatic; gene expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a secreted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                 related polynucleotide SEQ ID NO 408
                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Graham JR;
                                                                                                                                                                                   cancer; tumour; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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                                                                                                                                                                                         gene mapping; tissue profiling;
ss.
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57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Resnick
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RESULT 19
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          WPI; 2001-433142/47
                                  Regenbogen J, Wolf E,
                                                                                                17-NOV-1999;
17-DEC-1999;
                                                                                                                                                              17-MAY-2001.
                                                                                                                                                                                      CA2325226-A1
                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                     gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                          1080 GAAGGTGGAGCTGGCAGGA 1098
                                                           (SWIT-) SWITCH BIOTECH AG
                                                                                    20-JUN-2000;
                                                                                                                                    16-NOV-2000; 2000CA-2325226.
                                                                                                                                                                                                                                                                         Human wound healing related polynucleotide SEQ ID NO 97
                                                                                                                                                                                                                                                                                                      25-JAN-2002
                                                                                                                                                                                                                                                                                                                              ABA82018;
                                                                                                                                                                                                                                                                                                                                                    ABA82018 standard; cDNA; 637 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 629 BP; 172 A; 195 C; 90 G; 172 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated polynucleotide (ABN27253-ABN33262) with cytostatic activity. The polynucleotide is used to produce a polypeptide, to detect differentially expressed genes correlated with a cancerous state of a mammalian cell and to inhibit tumour growth. The polynucleotide is used as a probe in mapping and tissue profiling. The encoded polypeptide and antibodies to the polypeptide can also be used for therapeutic and diagnostic purposes. The polynucleotide is useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 408; 883pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid for producing a polypeptide, detecting different expressed genes correlated with a cancerous state of a mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and inhibiting tumor growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-241905/29.
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Lamson G, Scott
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CHIR ) CHIRON CORP. (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-AUG-2000; 2000US-226326P
                                                                                                                                                                                                                                                                                                                                                                                                                 253 GAAGGTGGAGCTGGCAGGA 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                    mouse;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                   2000DE-1030149
                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Garcia PD,
                                                                                                                                                                                                                                         SS.
                                                                                                                                                                                                                                               vulnerary; dermatological; skin disorder; wound healing;
                                                                                                99DE-1055349
99US-0172511
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                                 Goppelt A,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 19;
Pred. No.
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                               Werner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB
57;
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                                 Halle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 629;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                anticonvulsant; antiarthritic; cereproprocective, uncleased antiasthmatic; antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic; thrombolytic; immunogen; antibody; gene therapy; neurological disorder; thrombolytic; immunogen; antibody; disorder; cancer; asthma; osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Note: The printed sequence listing for this specification was incomplete, terminating part way through SEQ ID NO 106. The remaining data was obtained from EPO data for an equivalent patent (EP1114862).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB44606-ABB44623) or its variant or encoding nucleic acid (ABA81990-ABB4995, ABA82016-ABB82032) with vulnerary and/or dermatological activity for the diagnosis, prevention and treatment of skin disorders and treatment in wound healing or for the identification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 243-244; 265pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       substances
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; novel protein; ss; Antianaemic; osteopathic; antiinflammatory; immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic; anticonvulsant; antiarthritic; cerebroprotective; antifungal; antivir;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAS22581 standard; cDNA; 737 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 637
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Claim 1; Page 375-376; 894pp; English.
                                                                                                                                                                                                                                                                                                                                                                                       25-JAN-2000; 2000US-0491404
                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-JAN-2001; 2001WO-US02623.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200155437-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-OCT-2001 (first entry)
                                                               nervous system disorders, and
                                                                                                                                                                                                                                                                                                                     (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            908 GGGAGCAGGAGGAGAAGTT 926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 GGGAGCAGGAGGAGAAGTT 44
                                                                                                                                                                                             2001-451939/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA encoding a novel human protein #147.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             regeneration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                            AAU14276
                                                               polypeptides useful for treating anti-inflammatory diseases,
system disorders, and for regenerating bone and cartilage -
                                                                                                                                                                                                                                                         Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                            Drmanac RT;
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Pred. No.
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The invention relates to polynucleotides encoding novel human proteins or their active domains. The polypeptides, polynucleotides and antibodies raised against the polypeptides are used in a method of

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В
Job time
                   Search completed: December
                                                                                                                                                                                                            Best
                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein expression or activity. The polypeptides can be used as molecular weight markers, food supplements, and in antibody production. The polypeptides are used to identify compounds which bind to the polypeptides. Polynucleotides of the invention are used as probes and primers, for sequencing, for chromosome or gene mapping, in the production of recombinant proteins, and in generating anti-sense DNA or RNA and in gene therapy. Polypeptides of the invention can be used to target drugs to a tumour, in assays to determine biological activity, to
                                                                                                                                                                                                                                                                                                                                                                                                                 raise antibodies/elicit an immune response, to determine quantitative protein levels, as tissue markers, and to isolate receptors or ligands. Polypeptides of the invention may also be useful in treating platelet disorders, stem cell disorders, regenerating bone, cartilage, tendon, ligament and/or nerve tissue, wound healing, treating burns, promoting the proliferation, differentiation and survival of stem cells, as a contraceptive, treating osteoporesis and osteoarthritis, anaemia, alzheimer's, Parkinson's and Huntington's diseases, amylotrophic lateral sclerosis, stroke, immune deficiences resulting from bacterial, viral of from antigeness resulting from bacterial, viral or from autofunctors responsed.
                                                                                                                                       1115 ATGAGAGCATGGAGCAATT 1133
                                                                                                                                                                                                                                                                                                                                                    graft-versus-host disease, eczema, haemophilia, thrombosis,
anti-inflammatory diseases, nervous system disorders, and infection.
                                                                                                                                                                                                                                                                               Sequence 737
                                                                                                                                                                                                                                                                                                                                                                                                   fungal infection or from autoimmunity, cancer, allergy, asthma,
                                                                                        699
                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                              present sequence encodes a protein of the invention
                                                                                      ATGAGAGCATGGAGCAATT 717
309 secs
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19; Conserv
                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                               BP; 246 A; 111 C; 146 G; 234 T; 0
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                   2002, 10:41:33
                                                                                                                                                                                                          Score 19;
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57;
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Title:
Perfect score:
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Word size :
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                                                                                                                                                                                                                                                                                                                                                                                                                    Database :
Published_Applications_Na:*

1: //ggn2_6/ptodata//pubpna/US07_PUBCOMB.seq:*
2: //cgn2_6/ptodata//pubpna/US06_NEW_PUB.seq:*
3: //ggn2_6/ptodata//pubpna/US06_NEW_PUB.seq:*
4: //ggn2_6/ptodata//pubpna/US06_NEW_PUB.seq:*
5: //ggn2_6/ptodata//pubpna/US07_NEW_PUB.seq:*
6: //ggn2_6/ptodata//pubpna/US08_NEW_PUB.seq:*
7: //ggn2_6/ptodata//pubpna/US08_NEW_PUB.seq:*
8: //ggn2_6/ptodata//pubpna/US08_PUBCOMB.seq:*
9: //ggn2_6/ptodata//pubpna/US09_PUBCOMB.seq:*
10: //ggn2_6/ptodata//pubpna/US09_PUBCOMB.seq:*
11: //ggn2_6/ptodata//pubpna/US10_NEW_PUB.seq:*
12: //ggn2_6/ptodata//pubpna/US10_NEW_PUB.seq:*
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Gapop 60.0 , Gapext 60.0
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1431
1 aaggagtgtaqacac
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

19	c 18	17	c 16	15	14	c 13	12	c 11	c 10	9	8	7	on	ი Մ	4	ω	٦(3	Result No.
17	17	17	18	18	18	18	18	18	18	18	18	18	19	19	27	27	28	1431	Score
1.2	1.2	1.2	1.3	1.3	1.3	1.3	1.3	1.3	1.3	μ. ω	1.3	1.3	1.3	1.3	1.9	1.9	2.0	100.0	Query Match
230	192	133	684973	4153	3033	860	746	467	467	445	444	399	2513	488	1762	587	1597	1431	Query Match Length
10	10	10	10	10	12	10	10	9	9	10	10	10	10	10	10	10	10	10	DB
US-09-864-761-22504	US-09-878-574-9448	US-09-776-695-22	US-09-263-959-1	US-09-917-800A-1593	US-10-044-090-508	US-09-833-381-303	US-09-822-849A-580	US-09-902-941-753	US-09-736-457-753	US-09-917-800A-577	US-09-960-352-13152	US-09-960-352-207	US-09-822-849A-268	US-09-917-800A-81	US-09-764-864-34	US-09-764-864-493	US-09-908-988B-5	US-09-908-988B-1	ID
Sequence 22504, A	Sequence 9448, Ap	Sequence 22, Appl	Sequence 1, Appli	Sequence 1593, Ap	Sequence 508, App	Sequence 303, App	•	Sequence 753, App				Sequence 207, App	Sequence 268, App	Sequence 81, Appl	Sequence 34, Appl	Sequence 493, App	Sequence 5, Appli	Sequence 1, Appli	Description

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1041 1043 1048	774 815	570 588	488 497 535	465 485	446 459	347 370 417	286 292 295	231 262 264 264
10	10	10	10	10	10 10	10 10	10	100
US-09-974-300-523 US-09-778-844-129 US-09-778-844-130 US-09-822-849A-117	US-09-764-864-40 US-09-818-954A-18	US-09-864-761-14784 US-09-768-020-75	US-09-864-761-15156 US-09-783-590-8999 US-09-974-300-3014	US-09-864-761-6101 US-09-864-761-5742	US-09-764-864-482 US-09-864-761-31683	US-09-864-761-22849 US-09-960-352-2716 US-09-867-701-4631	US-09-294-093B-1812	US-09-923-876-2132 US-09-878-574-8578 US-09-294-0938-2808 US-09-764-864-499 US-09-764-864-499
Sequence 129, App Sequence 130, App Sequence 137, App	18,		Sequence 13136, A Sequence 8999, Ap Sequence 3014, Ap		- ~	Sequence 22849, A Sequence 2716, Ap Sequence 4631, Ap	10927 1300, 1812,	Sequence 2132, Ap Sequence 8578, Ap Sequence 2808, Ap Sequence 499, App Sequence 5150, Ap

ALIGNMENTS

QY 121 TGACCGAGGAAGGTGCACAGGCAGGGAGAAGGCCAACGACAAGGGCACAGCGAGGCAG 1	QY 1 AAGGAGTGTAGACAGAGTGTCTGGAAATAGACAGGGGTGAGAGGAGCTGTTAGGGGAAGG 6	Query Match 100.0%; Score 1431; DB 10; Length 1431; Best Local Similarity 100.0%; Pred. No. 0; Matches 1431; Conservative 0; Mismatches 0; Indels 0; Gap:	Sequence 1, Application US/0990898B Patent No. US2020217690A1 GENERAL INFORMATION: APPLICANT: OLSON, ERIC APPLICANT: SPENCER, JEFFREY A. APPLICANT: SPENCER, JEFFREY A. APPLICANT: SPENCER, JEFFREY A. APPLICANT: SPENCER, JEFFREY A. APPLICATION: MCTHODS AND COMPOSITIONS FOR STABILIZING MICROTUBE TITLE OF INVENTION: IN STRIATED MUSCLE CELLS FILLE REFERENCE: MYOG:028US CURRENT APPLICATION NUMBER: US/09/908,988B CURRENT APPLICATION NUMBER: 60/219,020 PRIOR APPLICATION NUMBER: 60/219,020 PRIOR FILING DATE: 2000-07-18 NUMBER OF SEQ ID NOS: 6 SOFTWARE: PATENTIN VOI: 2.1 SEQ ID NO 1 LENGTH: 1431 TYPE: DNA ORGANISM: Mus musculus FEATURE: NAME/KEY: CDS LOCATION: (199)(1296)
GCAG 180 GCAG 180	PAAGG 60 PAAGG 60 PAAAC 120 PAAAC 120	1;); Gaps 0	MICROTUBULES

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            1261 GAGCGGCTGGACGTGCCAGAAGGCTCAGGCCTGCACTGACCCGACTCTGATCCAGAGCGC
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                                  GATGAAGAGGATGACGACATGGCTTTGGATGGGGAGGAGGGCAATGCGGGGGCTGGAGGAG
                                                                                                                                                                                                                                                         CTGGCCCGGGAGCAGGAGGAGGAGTTGCAGCGCGTGCGGGGGCCTCATCCGCCAGTACGGA 960
                                                                                                                                                                                                                                                                                                   CAGAGGTTCGAGACCCTGTGCGCGGTTTTGGAGGAGGGCGAAGGGCGAACTGCTTCAAGCA 900
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                                                                                                                         AAGGTGGAGCTGGCAGGACGCCGGAGCCAGGCTATGAGAGCATGGAGCAATTCTCTGTG
                                                                                                                                      AAGGTGGAGCTGGCAGGACGGCCGGAGCCAGGCTATGAGAGCATGGAGCAATTCTCTGTG
                                                                                                                                                                                                                           GACCACTTGGAGGGCTCCTCAAAGCTGGTGGAGTCCGCCATCCAGTCCATGGAGGAGCCG 1020
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AGCGTGGAGCACGTGGCCGAAATGTTGCGAACCATCGACTTCCAGCCGGGCGCCGCTGGG
                                                                                                                                                                    CAGATGGCTCTCTACCTCCAGCAGGCAAAGGAGCTGATCAACAAGGTCGGGGCAATGTCG
                                                                                                                                                                                         CAGATGGCTCTCTACCTCCAGCAGGCAAAGGAGCTGATCAACAAGGTCGGGGGCAATGTCG
                                                                                                                                                                                                              GACCACTTGGAGGGCTCCTCAAAGCTGGTGGAGTCCGCCATCCAGTCCATGGAGGAGCCG
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                                                                                                                                                                                                                         SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 493
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 493, Application US/09764864 Patent No. US20020132753A1
                                                                            Matches
                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
                                                                                                                                                                                                                                                                   APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PTZ23
CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
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Best Local (
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APPLICANT: SPENCER, JEFFREY A.
APPLICANT: SPENCER, JEFFREY A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STABILIZING MICROTUBULES
TITLE OF INVENTION: IN STRIATED MUSCLE CELLS
FILE REFERENCE: MYOG:028US
CURRENT APPLICATION NUMBER: US/09/908,988B
CURRENT FILING DATE: 2000-07-18
PRIOR FALING DATE: 2000-07-18
PRIOR FALING DATE: 2000-07-18
                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 1792
                                                                                                                                                                LENGTH: 587
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: CDS
LOCATION: (299)..(1327)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1597
                 508 ATCATTGACATCTACAAGCAGGAGTCC 534
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                                                                                          Local
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                                                                                          Similarity
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                                                                      1.9%; Score 27; llarity 100.0%; Pred. No. Conservative 0; Mismatch
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                                                                      Mismatches
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                                                                                    DB 10;
0.00052;
                                                                                                        Length 587;
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                                                                    Indels
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                                                                  Gaps
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; TYPE: DNA; Homo sapiens; ORGANISM: Homo sapiens US-09-764-864-34
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US-09-917-800A-81/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/917,800A
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/22,040
PRIOR FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: US 60/222,880
PRIOR FILING DATE: 2000-11-02
PRIOR PILING DATE: 2000-105-11
PRIOR PILING DATE: 2001-05-11
PRIOR PILING DATE: 2001-05-12
PRIOR APPLICATION NUMBER: US 60/290,645
PRIOR APPLICATION NUMBER: US 60/290,645
PRIOR APPLICATION NUMBER: US 60/292,336
PRIOR FILING DATE: 2001-05-22
PRIOR FILING DATE: 2001-05-22
PRIOR FILING DATE: 2001-05-22
                                                                           US-09-917-800A-81
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SEQ ID NO 81
LENGTH: 488
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CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 1792
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5028-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/303,459
PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 1740
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/295,798 PRIOR FILING DATE: 2001-06-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1762
                                                                                                                                                                        TYPE: DNA
                                                                                                  OTHER INFORMATION: Genbank Accession No. US20020119462A1 AA818770
                                                                                                                          FEATURE:
                                                                                                                                              ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            467 ATCATTGACATCTACAAGCAGGAGTCC 493
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                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 60/297,457 FILING DATE: 2001-06-13
                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 60/298,884 FILING DATE: 2001-06-19
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Castle, Arthur
Elashoff, Michael
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  1.3%;
  Score 19;
Pred. No.
     DB 10;
6.2;
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US-09-822-849A-268
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LENGTH: 2513
TYPE: DNA
ORGANIEM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 268, Application US/09822849A Patent No. US20020045170Al
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                                                                                                                                                                                                                                      SEQ ID NO 207
LENGTH: 399
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                                     Query Match
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APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
APPLICANT: Mathialagan, Nagappan
APPLICANT: MATHIALAGAN, NAGAPPAN
TITLE OF INVENTION: MUSCLE AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
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TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
FILE REFERENCE: GIN 6403
CURRENT APPLICATION NUMBER: US/09/822,849A
CURRENT FILING DATE: 2001-09-04
PRIOR APPLICATION NUMBER: 60/195,582
PRIOR APPLICATION NUMBER: 60/195,582
PRIOR FILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 598
SOFTWARE: Patentin Ver. 2.0
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Best Local Similarity
Matches 18; Conserv
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                                                                                     NAME/KEY: unsure
LOCATION: (359)
OTHER INFORMATION: unsure at all n locations
OTHER INFORMATION: Clone ID: 01-LIB34-072-Q1-E1-A1
                                                                                                                                                                                              TYPE: DNA
ORGANISM: Bos taurus
                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   137 CACAGGCAGGGGAGAAGGC 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            390 TGGGGATGAAGAGGATGAC 372
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Gulukota, Kamalakar
Graham, James R.
Genetics Institute,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Agostino, Michael J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.3%; Score 19; DB 10; Length 2513; 100.0%; Pred. No. 6.3;
              1.3%; Score 18; DB 10; Length 399; 100.0%; Pred. No. 20;
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  Mismatches
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      Gaps
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US-09-917-800A-577
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APPLICANT: Tao, Nenghing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECU
TITLE OF INVENTION: MUSCLE AND EAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
COURRENT FILING DATE: 2001-09-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Qy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 13152
LENGTH: 444
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Patent No. US20020137139A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5038-US
CURRENT APPLICATION NUMBER: US/09/917,800A
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/222,040
PRIOR FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: US 60/222,880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
PRIOR APPLICATION NUMBER: US 6
PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 1740
SOFTWARE: PATENTIN VEr. 2.1
SEQ ID NO 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Bos taurus
OTHER INFORMATION: Clone ID: 56-LIB34-001-Q1-E1-F8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            795 CCAGACCATTGAGGACAA 812
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les 18; Conserv
                                                                                                                                                                                                                                      APPLICATION NUMBER: US 60/290,645
FILING DATE: 2001-05-15
APPLICATION NUMBER: US 60/292,336
FILING DATE: 2001-05-22
                                                                                                          APPLICATION NUMBER: US 60/298,884 FILING DATE: 2001-06-19
                                                                                                                                                                     APPLICATION NUMBER: US 60/297,457
                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 60/290,029 FILING DATE: 2001-05-11
                                                                                                                                                     FILING DATE: 2001-06-13
                                                                                                                                                                                                                  APPLICATION NUMBER: US 60/295,798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Castle, Arthur
Elashoff, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Johnson, Kory
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                                                                                                                                                                                              2001-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 18;
100.0%; Pred. No. .
tive 0; Mismar
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                                                                                   60/303,459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(467)
; OTHER INFORMATION: n = A,T,C or G
US-09-736-457-753
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                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                     Sequence 75 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/736,457
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 1864
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 753
                                                        APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                 Matches
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              APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT:
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APPLICANT:
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APPLICANT: Wang, Ajjun
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
  APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 467
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Rattus norvegicus FEATURE:
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TYPE: DNA
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                                                                                                                                                                                                                                                       442 CTCTCTCTGCAAGGTTTT 425
                                                                                                                                                                                                                                                                                  636 CTCTCTCTGCAAGGTTTT 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           212 CCAAGCTCGGCTTCCCGC 229
                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                    753, Application US/09902941 o. US20020172952A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION
                                                                                                                                                                                                                                                                                                               18;
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US20020168637A1
                                                                                                                                         Henderson, Robert A.
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Bangur,
McNabb,
                       Fanger, Gary R. Vedvick, Thomas
                                                     Marnerakis, Margarita
Carter, Darrick
                                                                                                             Wang, Tongtong
Watanabe, Yoshihiro
                                                                                  Retter, Marc W.
                                                                                              Johnson,
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Retter, Marc
Mannion, Jane
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Vedvick, Tom
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Lodes, Michael
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           Chaitanya S
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                            Thomas S
                                                                                                Jeffrey C.
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Pred. No.
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Pred. No.
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NAME/KEY: misc_feature; LOCATION: 1, 15, 77, 314, 317, 335, 419; OTHER INFORMATION: n = A,T,C or GUS-09-902-941-753
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US-09-822-849A-580
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PATERIC INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION: Wo. US20020132090A1el Nucleic Acid and Protein Homologs:
TITLE OF INVENTION: NO. US20020132090A1el Nucleic Acid and Protein Homologs:
FILE REFERENCE: 5800-119
CURRENT APPLICATION NUMBER: US/09/833,381
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APPLICANT:
                                                                                                                                                  sequence 303, Application US/09833381
Patent No. US20020132090A1
                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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LENGTH: 746
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/195,582
PRIOR FILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 598
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Wong, Gordon G. APPLICANT: Clark, Hilary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/822,849A CURRENT FILING DATE: 2001-09-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
FILE REFERENCE: GIN 6403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                   GCCCGGGAGCAGGAGGAG 422
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Fechtel, Kim
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                                                                                                                                                                                                                                                                                                                                                 Conservative
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100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                  100.0%;
                                                                                                                                                                                                                                                                                                                                                                1.3%; Score 18; DB 10; Length 746; 100.0%; Pred. No. 20;

 Mismatches

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                                                                                                                                                                                                                                                                                                                                               Mismatches
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20;
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(860)
; OTHER INFORMATION: n = A,T,C or
US-09-833-381-303
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; OTHER INFORMATION: Incyte ID No. US20020137081A1 082155CB1
US-10-044-090-508
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APPLICANT: Elashoff, Michael
APPLICANT: Gene Logic, Inc.
FITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5038-US
CURRENT APPLICATION NUMBER: US/09/917,800A
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/222,040
PRIOR APPLICATION NUMBER: US 60/222,880
PRIOR APPLICATION NUMBER: US 60/222,880
PRIOR APPLICATION NUMBER: US 60/222,880
PRIOR APPLICATION NUMBER: US 60/290,029
                                                                                                                                                                                                                                                                                                                                                               RESULT 15
US-09-917-800A-1593
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Olga Bandman
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                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Mendrick, Donna
                                                                                                                                                                                                                                                                                                                   Sequence 1593, Application US/09917800A
Patent No. US20020119462A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION FILE REFERENCE: PA-0028 US CURRENT APPLICATION NUMBER: US/10/044,090 CURRENT FILING DATE: 2002-01-09 NUMBER OF SEQ ID NOS: 850
SOFTWARE: PERL Program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 09/516,448
PRIOR FILING DATE: 2000-02-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 3033
TYPE: DNA
ORGANISM: Homo sapiens
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nes 18; Conserv
                                                                                                                                                                                                    Johnson, Kory
Castle, Arthur
Elashoff, Michael
                                                                                                                                                                                                                                                               Porter, Mark
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100.0%; Pred. No.
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100.0%; Pred. No.
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FILING DATE: 2001-05-11
APPLICATION NUMBER: US 60/290,645
FILING DATE: 2001-05-15

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US-09-263-959-1
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Patent No. US20020150891A1
GENERAL INFORMATION:
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Best Local Similarity 100.0%;
Matches 18; Conservative
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SEQ ID NO 1593
LENGTH: 4153
                                                            TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 684973 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/303,459
PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 1740
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PRIOR FILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: US 60/295,798
PRIOR FILING DATE: 2001-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298,884
PRIOR FILING DATE: 2001-06-19
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ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Rowen, Lee APPLICANT: KOOP, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
                                                                                                                                        REFERENCE/DOCKET NUMBER: 92
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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STREET: Seattle
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               STRANDEDNESS: Si
TOPOLOGY: linear
                                                    TYPE:
                                                                                                                                                                                                NAME: McMasters, David REGISTRATION NUMBER: 3:
                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 05-MA
                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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                                              nucleic acid
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                               single
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Pred. No.
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; GENERAL INFORMATION:
                                                                                                                                       RESULT 18
US-09-878-574-9448/c
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US-09-776-695-22
                                                                                                   Sequence 9448, Application US/09878574 Patent No. US20020110548A1
                                                                                                                                                                                                                                                                                     Matches
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APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
                                                                                                                                                                                                                                                                                                    Best Local
                                                                                                                                                                                                                                                                                                                     Query Match
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INFORMATION FOR SEQ ID NO: 22:
                                                                                                                                                                                                                                              1007 CCATGGAGGAGCCGCAG 1023
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 01107.03170 TELECOMMUNICATION INFORMATION: TELEPHONE: 202-508-9100
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE DESCRIPTION: SEQ ID NO: 22:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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ADDRESSEE: Banner & Witcoff
STREET: 1001 G Street, NW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: NUCLEIC ACIDS ENCODING P53
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                                                                                                                                                                                                                                                                                     17; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 133 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/776,695
FILING DATE: 26-Feb-2001
CLASSIFICATION: CUNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 202-508-9299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Kagan, Sarah A
REGISTRATION NUMBER: 32141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Washington
                                                                                                                                                                                                                                                                                    Conservative
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100.0%; Pred. No.
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100.0%; Pred. No.
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; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION UNMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 9448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 701102502H1
US-09-878-574-9448
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PRIOR
PRIOR
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                                                                                                                        PRIOR
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TYPE: DNA
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nes 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 60/207,456
FILING DATE: 2000-05-26
APPLICATION NUMBER: US 09/632,366
FILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 60/180,312 FILING DATE: 2000-02-04
                                                                                                                                                                                                                                                                                          FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00568
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/US01/00667 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 60/236,359 FILING DATE: 2000-09-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: GB 24263.6 FILING DATE: 2000-10-04
APPLICATION NUMBER: US 60/234,687 FILING DATE: 2000-09-21 APPLICATION NUMBER: US 09/608,408 FILING DATE: 2000-06-30 APPLICATION NUMBER: US 09/774,203 FILING DATE: 2001-01-29
                                                                                                                                                                                                           APPLICATION NUMBER: PCT/US01/00662 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/US01/00663 FILING DATE: 2001-01-30
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Chen, Wensheng
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; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020013958a1 700160095H1
; NAME/KEY: unsure
; LOCATION: 190, 220
; OTHER INFORMATION: a, t, c, g, or other
US-09-923-876-2132
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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 22504
LENGTH: 230
                                                                                                                                                                                                                                                                                      SOFTWARE: PERL Program SEQ ID NO 2132 LENGTH: 231
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CURRENT FILING DATE: 2001-08-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Kamigaki, Laura Y. (Ito)
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYUCILEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
FILE REFERENCE: PL-0012-1 CON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Lalgudi, Raghunath V. APPLICANT: Kamigaki, Laura Y. (Ito) APPLICANT: Sherman, Bradley K.
                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 1999-0 PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 6332
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N: EXPRESSED IN HELR, SIGNAL = 2.7

N: EXPRESSED IN HEART, SIGNAL = 2.7

N: EXPRESSED IN FETAL LIVER, SIGNAL = 2.

N: EXPRESSED IN ADULT LIVER, SIGNAL = 2.

N: EXPRESSED IN BARIN, SIGNAL = 2.

N: EXPRESSED IN BARIN, SIGNAL = 1.

N: EXPRESSED IN BONE MARROW, SIGNAL = 1.

N: NT HIT: X84060.1, EVALUE 1.00e-127

N: SWISSPROT HIT: Q14494, EVALUE 1.00e-3

N: EST_HUMAN HIT: BE897190.1, EVALUE 1.0
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NUMBER: 60/085,331
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

RESULT 1	
AX418848	
LOCUS	AX418848 1431 bp DNA linear PAT 18-JUN-2002
DEFINITION	Sequence 1 from Patent WO0206318.
ACCESSION	AX418848
VERSION	AX418848.1 GI:21523712
KEYWORDS	
SOURCE	house mouse.
ORGANISM	Mus musculus
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	1
AUTHORS	Olson, E.N. and Spencer, J.A.
TITLE	Methods and compositions for stabilizing microtubules and
	intermediate filaments in striated muscle cells

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CACAAGGACTGTGAGGTGGCCCCTCTGCCCACCATTTACAAACGCCAGAAGAGTGAGCTG
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                                                           CCACTGCACGCCAAGGCTGAACAGCACCTCATGTGTGAGGAGCACGAGGACGAGAAGATC
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BOARD OF
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F REGENTS THE UNIVERSITY OF TEXAS SYSTEM (US)
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NLCRKCANDVFQASNPLMQSGGTSGSGTSGSCEREVLLDRGVVGLQRNLLEV
NIIDIYKQESSRPLHAKARQHLMCEGHEDEKINIYCLSCERUFYCSLGKVFQAHKDCEV
APLPTIYKRQKSELSDGIAMLVAGNDRVQAVITQMEEVCQTIEDNSRRQKQLLNQRFE
TLCAVLDERKGELLQALAREQEEKLQRVRGLIRQYGDHLEGSSKLVESAIQSMEEPQM
ALYLQQAKELINKVGAMSKVELAGREPEGYESMEQFSVSVEHVAEMLRTIDFQPGAAG
DEEDDDMALDGEEGNAGLEEERLDYPEGSGLH"
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Direct Submission
Submitted (09-AUG-2000) Molecular
Blvd., Dallas, TX 75390-9148, USA
                                              2 (bases 1 to 1448)
Spencer, J.A. and Olson,
                                                                                                                           MURF,
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NIIDIYQGESSRPLHAKAEQHLMCEBHEDEKINIYCLSCEVPFCSLCKVFGAHKDCEV
APLPTIYKRQKSELSDGIAMLYAGNDRVQAVITQMEEVCGIPEDNSRROKQLLNGRFE
TLCAVLEERKGELLQALARQDEEKLQRVRGLIRQYGDHLEGSSKLVESSAGUSMEEPQM
ALYLQQAKELLNKVGAMSKVELAGRPEDGYESMEQFSVSVEHVAEMLRTIDFQPGAAG
DEEDDDMALDGEEGNAGLEEERLDVPEGSGLH"
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/protein_id="AAG03076.1"
/db_xref="GI:9945010"
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/db_xref="taxon:10090"
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                                                                                                       Centher, T., Yano, J., Kimura, E., McElhinny, A.S., Pelin, K., Witt, C.C., Bang, M.L., Trombitas, K., Granzier, H., Gregorio, Sorimachi, H. and Labeit, S. Identification of muscle specific ring finger proteins as regulators of the titin kinase domain J. Mol. Biol. 306 (4), 717-726 (2001)
Submitted (12-FEB-2001) Centner T., Structure and Biocomputing EMBL-Heidelberg, Meyerhofstrasse 1, Heidelberg 69112, Germany
                                              Centner, T
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LWQsRcSTTVsSGGRFRcPsCReheVvLDRHGVVGLQRKLLVENIIDIYKQESSRPLHS
KAEQHLWCEHEEEEKINIYCLSCEVPTCSLCKVFGAHKDCEVAPLPTIYKRQKNELSD
GIAMLVAGNDRVEGVITQMEEVCQTIEDNSRRQKQLLTQRFESLCAVLEERKGELDSD
GIAMLVAGNDRVQAVITQMEEVCQTIEDNSRRQKQLLTQRFESLCAVLEERKGELDSD
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/translation="MDNLEKQLICPICLEMFSKPVVILPCQHNLCRKCANDVFQASNP
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TQMEEVCQTIEDMSRRQKQLLTQRFESICAVLEERKGEILQALAREQEEKLQRVRGLI
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         GCCCCCGGGAAGGTTCTCAATAAAGGACTCAAGTGTCC 1430
                                                                                                                      GTGCCAGAAGGCTCAGGCCTGCACTGACCCGACTCTGATCCAGAGCGCACACCCGAAGCG
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CGGCCCCGGGAGGATCTCAATAAAGAACTCGAGCGTCC
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                                  AAACCAGAGGTTTGAGAGCCTGTGCGCAGTGCTGGAGGAGCGCAACGGTGAGCTGCTGCA
                                                     AAACCAGAGGTTCGAGACCCTGTGCGCGGTTTTGGAGGAGCGCAAAGGGCGAACTGCTTCA 896
                                                                                                ACAGATGGAGGAGGTGTGCCAGACTATCGAGGACAATAGCCGGAGGCAGAAGCAGTTGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1500)
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                                                              CATGGTGTCTATGGCCTGCAGCGGAACCTGCTAGTGGAGAACATCATTGACATCTACAAG
                                                                                                                                                                                                                                                                                       TCCATGTCTGGAGGTCGTTTCCGTTGCCCCTCGTGCCGCCATGAAGTGATCATGGACCGG
                                                                                              CAGGAGTGCTCCAG---TCGGCCCCTGCAGAAAGGCAGCCACCCGATGTGCAAGGAACAC
                                                                                                                                                                         CAGGAGTCCTCCCGGCCACTGCACGCCAAGGCTGAACAGCACCTCATGTGTGAGGAGCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Methods and compositions for stabilizing microtubules intermediate filaments in striated muscle cells Patent: WO 0206318-A 5 24-JAN-2002; BOARD OF RECENTS THE UNIVERSITY OF TEXAS SYSTEM (US)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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/PIOTETI_Id="CAD35457.1"
/db_xref="GI:21523717"
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RKCANDIFQAANPYWTNRGGSVSMSGGRFRCPSCCHEVPIMDHGVYGLQRNLLVENII
DIYKQBCSSRPLQKGGSHPMCKBHEDEKINIYCLICDFVFRCSUSHQVKEDLSQKFDTVXB
SIFQGQKTELSNCISMLVAGNDRVQTIISQLBDSGRVTKENSHQVKEDLSQKFDTVXB
SIFQGQKTELSNCISMLVAGNDRVQTIISQLBDSGRVTKENSHQVKEDLSQKFDTVXB
SIFQGQKTELSNCISMLVAGNDRVQTIISQLBCKSTKLVETAIQSLDEPGGATFL
SSAKQLIKSIVEASKGCQLGKTEQGFENMDYFTLDLEHIAEALRAIDFGTGKGCDVTC
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                                                                                                                                           Submitted (12-FEB-2001) Centner T., EMBL-Heidelberg, Meyerhofstrasse 1, Revised by author 22\text{-}\text{FEB-2001}
                                                                                                                                                                                                                       Centner,
                                                                                                                                                                                                                                                                                     Identification of muscle specific ring finger proteins as potential regulators of the titin kinase domain J. Mol. Biol. 306 (4), 717-726 (2001)
                                                                                                                                                                                                                                                                                                                                          Centner, T., Yano, J., Kimura, E., McElhinny, A.S., Pelin, K., Witt, C.C., Bang, M.L., Trombitas, K., Granzier, H., Gregoric Sorimachi, H. and Labeit, S.
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                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
436. .438
                                                                                                               Location/Qualifiers
1. .2097
/evidence=not_experimental
475. .1497
                                 /note="putative alternative translation
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                                                                                                                                                                                                            ACCATCATCACTCAGCTGGAGGATTCCCCGTCGAGTGACCAAGGAGAACAGTCACCAGGTA
                                                                     GAGTTGCTGCAGCGGATCACGCAGGAGCAGGAGGAAAAGCTTAGCTTCATCGAGGCCCTC
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YWTSRCSSVSMSGRFFCCPTCHEVIMDRHGYVGLQRNLLVEBHIDIYKQECSSRPLQ
KGSHPMCKEHEDEKINIYCLTCEWFTCSMCKYFGIHKACEVAPLQSVFQGQKTELNNC
ISMLVAGNDRVQTIITQLEDSRRVTKENSHQVKEELSQRFDTLYAILDEKKSELLQRI
TQEQEERLSFTEALIQQYQEQLDKSTKLVETAIQSLDEPGGATFLLTAKQLIKSIVEA
SKGCQLGKTEQGFENNDFFTLDLEHIADALRAIDFGTDEEEEEFIEEEDQEEEESTEG
KEEGHQ"
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/protein_id="CAC33173.1"
/db_xref="GI:13171051"
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475. .1497
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/number=1
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                              /product="muscle specific RING finger 2 (MURF2)"
/product="muscle specific RING finger 2 (MURF2)"
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SVFQGQKTELNNCISMLVAGNDRVQTIITQLEDSRRVTKENSHQVKEELSQKFDTLYA
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                                                                                                                                                                                                                                                                                                                                                        /clone="STRAIT03036"
/tissue_type="skeletal muscle"
/clone_lib="pEAK8"
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/db_xref="taxon:9606"
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   ACCATCATCACTCAGCTGGAGGATTCCCGTCGAGTGACCAAGGAGAACAGTCACCAGGTA
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                                 TGGAGATGTTTACCAAGCCAGTGGTCATCTTGCCGTGCCAGCACCACCTGTGCCGGAAG
TGTGCCAACGACGTCTTCCAGGCCTCTAATCCTCTGTGGCAATCCCGGGGCTCCACAACG
                                                  CTGGAGATGTTCTCCCAAGCCCGTGGTGATCTTGCCCTGCCAACACAACCTGTGCCGCAAG 345
                                                                                                                                         CTGCTAGGGGATGCGCACAACATGGACAACTTGGAGAAGCAGCTCATTTGCCCCCATCTGC 285
                                                                                                       CTGATCCAGGATGGGAATCCCATGGAGAACTTGGAGAAGCAGCTGATCTGCCCTATCTGC 200
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Patent: WO 0172777-A 192 04-OCT-2001;
Incyte Genomics, Inc. (US)
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Sequence 192 from Patent W00172777
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/db_xref="taxon:9606"
/note="Incyte ID No: 3575519CB1"
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GAAGGGAAGGAAGGACCACCAGTAAGGAGCTGGATG 1195
                              GCGGGGCTGGAGGAGGAGCGGCTGGACGTGCCAGAAGG
                                                                    ACAGATGAGGAAGAAGAATTCATTGAAGAAGAAGATCAGGAAGAGGAAGAGTCCACA 1157
                                                                                                                                                            GAGCAATTCTCTGTGAGCGTGGACCACGTGGCCGAAATGTTGCGAACCATCGACTTCCAG 1185
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RESULT 9
AK056942
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LOCUS

AK056942

DEFINITION Homo sapiens cDNA FLJ32380 fis, clone SKMUS100064, moderately similar to Mus musculus RING-finger protein MURF mRNA.

ACCESSION AK056942

VERSION AK056942.1 GI:16552479

KEYWORDS Oligo capping; fis (full insert sequence).

SOURCE Homo sapiens skeletal muscle cDNA to mRNA, clone_lib:SKMUS1

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COMMENT
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TITLE
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  466 CATGGTGTCTATGGCCTGCAGCGGAACCTGCTAGTGGAGAACATCATTGACATCTACAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                       CTGGAGATGTTCTCCAAGCCCGTGGTGATCTTGCCCTGCCAACACAACCTGTGCCGCAAG 345
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                                                                                                           GTGTCTTCAGGAGGACGTTTCCGATGCCCATCTTGTAGGCACGAGGTTGTCCTGGACAGG
                                                                                                                                                                    TGTGCCAATGACATCTTCCAGGCTGCAAATCCCTACTGGACCAGCCGGGGCAGCTCAGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (24-OCT-2001) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomicsehri.co.jp, Tel.81-438-52-3975, Fax:81-438-52-3986) MEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center tc.); 5'-& 3'-end one pass sequencing: RAB, HRI, and Blotechnology Center National Institute of Technology and Evaluation; clone selection for full insert sequencing: RAB and
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Isogai,T., Otsuki,T. and Sugiyama,T.
Direct Submission
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ILDEKKSELLQRITQEQEKKLSFIEALIQQYQEQLDKSTKLVETAIQSLDEPGGATFL
LTAKQLIKSIVEASKGCQLGKTEQGFENMDFFTLDLEHIADALRAIDFGTDEEEEEFI
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RKCANDIFQAANPYWTSRGSSVSMSGGRFRCPTCRHEVIMDRHGVYGLQRNLLVENII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="skeletal muscle"
/clone_lib="SKMUS1"
/note="cloning vector: pME18SF
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/db_xref="GI:16552480"
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JOURNAL AUTHORS

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AAGGAAGAGCTGAGCCAGAAGTTTGACACGTTGTATGCCATCCTGGATGAGAAGAAAGT
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                                                               ACCATCATCACTCAGCTGGAGGATTCCCCGTCGAGTGACCAAGGAGAACAGTCACCAGGTA
                                                                                                                                                                   CAGAAGAGTGAGCTGAGCGATGGCATCGCGATGCTGGTGGCGGGCAATGACCGTGTGCAG
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                                                                                                   GCAGTGATCACCCAGATGGAGGAGGTGTGCCAGACCATTGAGGACAACAGCCGCAGACAG
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/product="iris ring finger protein"
/product="iris ring finger protein"
/product="iris ring finger protein"
/db_xref="GG:13785924"
/translation="MDYKSSLIODGNPMENLEKQLICPICLEMFTKPVVILPCQHNLC
RKCANDIFOANPYMTSRGSSYSMSGGRFRCPTCRHEVIMDRHGVYGLQRNLLVENII
DIYKQECSSRPLOKGSHPMCKEHEDEKLNIVGLITCEVPTCSMCKVPGILKACEPAPLO
SVFQGGKTELNNCISMLVAGNDRVQTIITQLEDSRRVTKENSHQVKEELSQKFDTLYA
ILDEKKSELLQRITOSQEKKLSFIEALIQQYQEGLDKSTKLVETATQSLDEPGGATFL
LTAKQLIKSIVPASKGCQLGKTEGGFENMDFFTLDLEHIADALRAIDFGTDEEEEEFI
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                      Submitted (12-OCT-2001) Muscle Research, 777 Old Saw Mill River Road, Tarrytown, N Location/Qualifiers
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Rattus norvegicus
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                        /translation="MDYKSGLIPDGNAMENLEKQLICPICLEMFTKPVVILPCQHNLC
RKCANDIFQAANPYWTNRGGSVSMSGGRFRCPSCRHEVIMDRHGVYGLQRNLLVENII
DIYKQBCSSRPLQKGSHPMCKEHEDEKINIYCLTCEVPTCSLCKVFGAHQACEVAPLQ
                    SIFQGQKTELSNCISMLVAGNDRVQTIISQLEDSCRVTKENSHQVKEELSHKFDALYA
                                                                                                              /product="muscle ring finger protein 1"
/protein_id="AAL16405.1"
/db_xref="GI:16444656"
                                                                                                                                                                                                                                       /organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
ILDEKKSELLQRITQEQEEKLDFIEALILQYREQLEKSTKLVETAIQSLDEPGGATFL
                                                                                                                                                                             /codon_start=1
                                                                                                                                                                                            /note="MuRF1; monomeric E3 ubiquitin ligase"
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                                 AGCAATTCTCTGTGAGCGTGGAGCACGTGGCCGAAATGTTGCGAACCATCGACTTCCAGC 1186
                                                                          TTGTAGAAGCTTCCAAGGGCTGCCAGCTGGGGAAGACAGAACAAGGCTTTGAGAACATGG 1010
                                                                                                           TCGGGGCAATGTCGAAGGTGGAGCTGGCAGGACGGCCGGAGCCAGGCTATGAGAGCATGG 1126
                                                                                                                                               CCCTGGATGAGCCCGGAGGGGCCACCTTCCTCTTGAGTGCCAAGCCGCTCATCAAGAGCA 950
                                                                                                                                                                                    CCATGGAGGAGCCGCAGATGGCTCTCTACCTCCAGCAGGCAAAGGAGCTGATCAACAAGG 106
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (09-OCT-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BC015717
BC015717.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo sen Lee, Victor Ling, Carrie Matthewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BC015717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series; IRAK Plate: 15 Row: O Column: 19
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 14211914.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortiu DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clone distribution: MGC clone distribution information can be found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       George Yang, Scott Zuyderduyn, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   info@bcgsc.bc.ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Dases I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sapiens
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SVFQGOKTELNNCISMLVAGNDRVQTIITQLEDSRRVTKENSHQVKEELSQKFDTLYA
ILDEKKSELLQRITQEQEEKLSFIEALIQQYQEQLDKSTKLVETAIQSLDEPGGATFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="MGC:17320 IMAGE:3922363"
/tissue_type="Skin, melanotic melanoma."
/clone_lib="NIH_MCC_72"
/lab_host="DH10B"
                                                                                                                                  VDTKKQKTDEDD'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:9606"
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  33.2%;
68.1%;
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                                                                                                       345 g
     score 475.6; DB 9;
pred. No. 2.6e-82;
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                                Length 1211;
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4.	RESULT 13 AX418850	AX
Db 428 AAAAAAT	QY 1186 CCGGGCGCCGCTGGGGATGAAGAGGATGACGACA 1219	ДĄ
368 547	QY 1126 GAGCAATTCTCTGTGAGCGTGGAGCACGTGGCCGAAATGTTGCCGAACCATCGACTTCCAG 1185	pb Qy
308	QY 1066 GTCGGGGCAATGTCGAAGGTGGAGCTGGCAGGACGAGGCAGGC	ad V
248	QY 1006 TCCATGGAGGAGCCGCAGATGGCTCTCTACCTCCAGCAGGCAAAGGAGCTGATCAACAAG 1065	B 8
188	Qy 946 ATCCGCCAGTACGGAGACCACTTGGAGGGCTCCTCAAAGCTGGTGGAGTCCGCCATCCAG 1005	B 8
128	QY 886 GAACTGCTTCAAGCACTGGCCCGGGAGCAGGAGGAGAAGTTGCAGCGCGTGCGGGGCCTC 945	B 8
187	QY 826 AAGCAACTGTTAAACCAGAGGTTCGAGACCCTGTGCGCGGTTTTGGAGGAGGAGCGCAAGGGC 885	D S
Query Ma Best Loc Matches	Qy 766 GCAGTGATCACCCAGATGGAGGAGGTGTGCCAGACCATTGAGGACAACAGCCGCAGACAG 825	B 6
BASE COUNT ORIGIN	Qy 706 CAGAAGAGTGAGCGATGGCATCGCGATGCTGGTGGCGGGCAATGACCGTGTGCAG 765	Б 6
	QY 646 AAGGTTTTCGGCGCCCACAAGGACTGTGAGGTGGCCCCTCTGCCCACCATTTACAAACGC 705	ā ö
	586 510	<u> </u>
	Qy 526 CAGGAGTCCTCCCGGCCACTGCACGCCCAAGGCTGAACAGCACCTCATGTGTGAGGAGCAC 585	<u> </u>
CDS	QY 466 CATGGTGTCTATGGCCTGCAGCGGAACCTGCTAGTGGAGAACATCATTGACATCTACAAG 525	<u>D</u> 0
FEATURES source	QY 406 GTGTCTTCAGGAGGACGTTTCCGATGCCCATCTTGTAGGCACGAGGTTGTCCTGGACAGG 465	g o
	QY 346 TGTGCCAACGACGTCTTCCAGGCCTCTAATCCTCTGTGGCAATCCCGGGGGCTCCACAACG 405	ם פ
ORGANISM Mus Euka Mamm	Qy 286 CTGGAGATGTTCTCCAAGCCCGTGGTGATCTTGCCCTGCCAACACACAC	υ o
TION ION ION	CTGCTAGGGGATGCGCACAACATGGACAACTTGGAGAAGCAGCTCATTTGCCCCATCTGC 285	ם מ
	Matches 677; Conservative 0; Mismatches 314; Indels 3; Gaps 1;	

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PCTGAACTGTGAAGTGCCCACCTGTTCCTTGTGCAAGGTTTTTGGCGCCCATAAG
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smusculus
karyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
mmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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quence 3 from Patent WO0206318.
118850
18850.1 GI:21523714
                                     CTGAGCTGCGAGGTGCCCACCTGCTCTCTCTGCAAGGTTTTCGGCGCCCACAAG 666
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                                                                                                                                                           NTTGG-----ACCAGCCCATGTGTGAAGAGCATGAAGAGGAACGCATCAACATC
                                                                                                                                                                                                    AAGGCTGAACAGCACCTCATGTGTGAGGAGGAGGAGGAGGAGGAGGAGGATCAACATC 606
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/ COUGLE-GALT-1
/ PROTECTIE_GALT-1
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BC007750
                                                cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
                                                                                                                                                                                                                                Submitted (11-MAY-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer
                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                   Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                                                                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                                                                                         Strausberg,R
                Gaithersburg, Maryland
                                    Sequencing Center (NISC),
                                                                                                                                                                       NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                              Institute, 31 Center Drive, Room 11A03, Bethesda,
                                                                                                                                                                                                                                                                                                             (bases 1 to 1750)
http://www.nisc.nih.gov/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1750 bp
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IMAGE:4110783, mRNA,
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TACTGCCTGAGCTGCGAGGTGCCCACCTGCTCTCTCTGCAAGGTTTTCGGCGCCCCACAAG 666
                                                   ---GAAAAGAAATCCGACCAGCCCATGTGCGAGGAACATGAAGAGGAGCGCATCAACATC
                                                                                                     CACGCCAAGGCTGAACAGCACCTCATGTGTGAGGAGGACGAGGAGGAGAAGATCAACATC
                                                                                                                                                         AGGAACCTGCTGGTGGAAAATATCATTGACATCTACAAGCAGGAGTCCACCAGGCCA---
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This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: nisc_mgc@nhgri.nih.gov
Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.,
Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Tlongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clone distribution: MGC clone distribution information can be found
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/PIOUCE-UNIAGRO/750.1"
/PIOUCE-UNIAGRO/750.1"
/PIOUCE-UNIAGRO/750.1"
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/db_xref="GI:14043532"
/translation="MDNLEKQLICPICLEMFTKPVVILPCQHNLCRKCASDIFQASNP
/translation="MDNLEKQLICPICLEMFTKPVLCRULLVENIIDIYKQESTRPEKK
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YLPTRGGTTMASGGRFRCPSCHEVVLLCRYPTCSLCKVPGQAHKDCQVAPLTHVPGNRKSELSDGI
XDQPMCEHLERERRINIYCLNCEVPTCSLCKVPGQAHKDCQVAPLTHVFGNRKNEMTVOTT
AILVGSNDKYGVISQLEDTCKTIEECCRKQKQELCEKTPLYGILEBRKKNEMTVOTT
RTQEEKLEHVRALIKKYSDHLENVSKLVESGICPMDEPEMAVFLQNAKTLIKKISEAS
KAFQMEKIEHGYENMAHFTVULNREEKLIRELDFYREDEDEEEEGGBEEKEGBEEVG
KAFQMEKIEHGYENMAHFTVULNREEKLIRELDFYREDEDEEEEGGBEEKEGBEEVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="Muscle, r
/clone_lib="NIH_MGC_17"
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/db_xref="taxon:9606"
/clone="MGC:12836 IMAGE:4110783"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="Unknown (protein for MGC:12836)"
/protein_id="AAH07750.1"
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                                                                             TITLE
                                                                                                                                                                                                                     AUTHORS
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                                                              Mishi,T., Ota,T., Nakagawa,S., Senoh,A., Mizuguchi,H., Inagaki,H., Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K., Wagatsuma,M., Murakawa,K., Kanehori,K., Kakahashi-Fujii,A., Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S., Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T. MEDO human cDNA sequencing project
                                                  Unpublished
                                                                                                                                                                                                                                                                                                                          AK091728.1 GI:21750167
oligo capping; fis (full insert sequence).
Homo sapiens heart cDNA to mRNA, clone_lib:HEART2
                                                                                                                                                                                                                                                                                                                                                                                                       AK091728 1925 bp mRNA linear PR Homo sapiens cDNA FLJ34409 fis, clone HEART2001931, mo similar to Mus musculus RING-finger protein MURF mRNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7 Kazusa-Kamatrari, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3985) Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, Evaluation; clone selection for full insert sequencing: HRI and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and
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1 (bases 1 to 2202)
Centner, T., Yano, J., Kimura, E., McElhinny, A.S., Pelin, K., Witt, C.C., Bang, M.L., Trombitas, K., Granzier, H., Gregorio, C.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens mRNA for RNF29 gene for ring AJ291712
                                                                                                                                                                                                                                                                                                              Submitted (12-FEB-2001) Centner T., Structure and Biocomputing, EMBL-Heidelberg, Meyerhofstrasse 1, Heidelberg 69112, Germany Revised by author 22-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                               Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Biol. 306 (4), 717-726 (2001)
                          /product="ring finger protein 29"
/protein_id="CAC32840.1"
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AILVGSNDRVQGVISQLEDTCKTIEECCRKQKQELCEKFDYLYGILEERKNEMTQVIT
                                                                                                                                      /gene="RNF29"
                                                                                                                                                                                       181.
                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                        /codon_start=1
                                                                                                                          /note="alternative"
                                                                                                                                                                     /gene=
                                                                                                                                                                                                     /evidence=not_experimental
                                                                                                                                                                                                                   /note="putative alternative translation
                                                                                                                                                                                                                                                                                                 location/Qualifiers
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187 GAGCGCCGCGGGATGAACTTCACGGTGGGTTTCAAGCCGCTGCTAGGGGATGCGCACAAC
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TTCGAGACCCTGTGCGCGGTTTTGGAGGAGCGCAAGGGCGAACTGCTTCAAGCACTGGCC
                                              GACACCTGCAAAACTATCGAGGAATGTTGCAGAAAACAGAAACAAGAGCTTTGTGAGAAG
                                                                                       GACTGCCAGGTGGCTCCCCTCACTCATGTGTTCCAGAGACAGAAGTCTGAGCTCAGTGAT
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PVTQGEVVPTGSEQTTESETPVPAAAETADPLFYPSWYKGQTRKATTNPPCTPGSEGL
GQIGPPGSEDSNVRKAEVAAAAASERAAVSGKETSAPAATSQIGFEAPPLQGQAAAPA
SGSGADSEPARHIFSFSWLNSLNE"
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GEAVEVEEVENVQTEFPGEDENPEKASELSQVELQAAPGALPVSSPEPPPALPPAADA
PVTQIGFEAPPLQGQAAAPASGSGADSEPARHIFSFSWLNSLNE"
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SDQPMCEEHEEERINIYCLNCEVPTCSLCKVFGAHKDCQVAPLTHVFQRQKSELSDGI
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RTQEEKLEHYKALIKKYSDHLENVSKLVESGIQFMDEPEMAVFIQNAKTLLKKISEAS
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KAFQMEKIEHGYENMNHFTVNLNREEKIIREIDFYREDEDEEEEEGGEGEKEGEGEVG
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                                                                Is Isogai, T. and Yamamoto, J.

Direct Submission

L Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7

Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan

(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

NEDO human CDNA sequencing project supported by Ministry of

Economy, Trade and Industry of Japan; CDNA full insert sequencing:

Research Association for Biotechnology (RAB); CDNA library

Construction: Helix Research Institute (HRI) (supported by Japan

Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,

HRI, and Biotechnology Center, National Institute of Technology and

Evaluation; clone selection for full insert sequencing: HRI and

RAB; annotation: HRI and RAB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AK091310.1 GI:21749650 oligo capping; fis (full insert sequence).
HOMO sapiens normal dermal fibroblasts (Neonatal Skin) (NHDF2564) cDNA to mRNA, clone_lib:DFNES2 clone:DFNES2007332.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AK091310 2634 bp mRNA linear PRI 15-JUL. Homo sapiens cDNA FLJ33991 fis, clone DFNES2007332, moderately similar to Mus musculus RING-finger protein MURF mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NEDO human cDNA sequencing
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                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 2634)
/organism="Homo sapiens
                                                     Location/Qualifiers
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                              GCTCTCTACCTCCAGCAGGCAAAGGAGCTGATCAACAAGGTCGGGGCAATGTCGAAGGTG
CGGGAGCAGGAGGAGAAGTTGCAGCGCGTGCGGGGCCTCATCCGCCAGTACGGAGACCAC 966
                                                                  TTGGAGAACGTCTCAAAGTTGGTTGAGTCAGGAATTCAGTTTATGGATGAGCCCAGAAATG
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/note="cloning vector: pME18SFL3-primary culture,
dermal fibroblasts"
1 580 c 586 g 675 t
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(NHDF2564)"
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                                              GAGCGCCGCGGGATGAACTTCACGGTGGGTTTCAAGCCGCTGCTAGGGGGATGCGCACAAC 246
                                                                                         701;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (29-JUN-1999) Gautel M.S., Physikalische Biochemie, Max-Planck-Institut fuer molekulare Physiologie, Otto-Hahn-Strasse 11, Dortmund, 44227, GERMANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1810) Kelly.R., Neubauer,G. and Gautel,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AJ243488.1 GI:14588845 alternative splicing; signal transduction; titin zinc-finger anchoring protein; tizian.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gautel, M.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A novel RING finger protein associated with titin
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Homo sapiens titin zinc-finger a
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                                                                                                                 Similarity
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227. .15
                                                                                                                                                                                                                                                                                                                                                                                            /evidence=experimental /product="fittin zinc-finger anchoring protein" /protein_id="Cac43019.1" /protein_id="Cac43019.1" /db_xref="GI:14588846" /translation="MSASLNYKSFSKEQQTMDNLEKQLICPICLEMFTKPVVILPCQH /translation="MSASLNYKSFSKEQQTMNLEKQLICPICLEMFTKPVVILPCQH /translation="MSASLNYKSFSKEQQTMNLEKQLICPICLEMFTKPVVILPCQH /translation="MSASLNYKSFSKEQQTMNLEKQLICPICLEMFTKPVVILPCQH /translation="MSASLNYKSFSKEQQTMNLEKQLICPICLEMFTKPVVILPCQH /translation="MSASLNYKSFSKEQQTMNLEKQLICPICLEMFTKPVVILPCQH /translation="MSASLNYKSFSKEQQTMNLEKQLICPICLEMFTKPVVILPCQH /translation="MSASLNYKSF"" /translation="MSASLNYKSF" /translation="MSAS
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VSSPEPPPALPPAADAPVTQIGFEAPPLQGQAAAPASGSGADSEPARHIFSFSWLNSL
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FLQNAKTLLKKISEASKAFQMEKIEHGYENMNHFTVNLNREEKIIREIDFYREDEDEE
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LTHVFQRQKSELSDGIAILVGSNDRVQGVISQLEDTCKTIEECCRKQKQELCEKFDYL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /function="putative role in signal transduction"
/note="50kDa isoform"
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                                                                                                                 Score 447.4; DB 9; Pred. No. 7.6e-77;
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                                                                                            Mismatches 376;
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                                                                                                                                                                                                                                                                                                                                                          GACAGCGAGGAGATGAGCGCATCTCTGAATTACAAATCTTTTTCCAAAGAGCAGCAGACC 274
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CGCTGCCCATCCTGTAGACATGAAGTGGTTTTGGATAGACATGGGGTATATGGACTTCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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/product "titin zinc-finger anchoring protein"
/product "de" "CAC43020.1"
/protein_id="CAC43020.1"
/db_xref="GI:14588848"
/translation="MSASLAYKSFSKEQQTMDNLEKQLICPICLEMFTKPYVILPCQH
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NIIDIYKQESTRPEKKSDQPMCEEHEEERINIYCLNCEVFCSLCKVFGAHKDCQVAP
LTHVFQRGKSELSBGTALTVGSNDEVGQVISQLEETGCTKTGCCTKQVGLCEKFDYL
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FLQNAKTILKKISBASKAFQMEKIBHGYENNHFTVNLNREEKJIREIDBYBE
FLQNAKTILKKISBASKAFQMEKIBHGYENNHFTVNLNREEKJIREIDBYBE
FLQNAKTILKKISBASKAFQMEKIBHGYENNHFTVNLNREEKJIREIDBYBE
FLQNAKTILKKISBASKAFQMEKIBHGYENNHFTVNLNREEKJIREIDBYBE
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VSSPEPPPALPPAADAPVTQGEVVPTGSEQTTESETPVPAAAETADPLFYPSWYKGQT
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IGFEAPPLQGQAAAPASGSGADSEPARHIFSFSWLNSLNE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /evidence=experimental
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/note="60kDa isoform"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cell_type="cardiomyocyte"
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                                                                                                GAGGATGACGACATGGCTTTGGATGGGGAGGAGGGCCAATGCGGGGCTGGAGGAGGAGCGG 1266
                                                                                                                                                                                                             TTTCAGATGGAGAAAATAGAACATGGCTATGAGAACATGAACCACTTCACAGTCAACCTC 1168
                                                                                                                                                                                                                                                GAGCTGGCAGGACGGCCGGAGCCAGGCTATGAGAGCATGGAGCAATTCTCTGTGAGCGTG 1146
TAGAA 1291
                                                                 GAAGAAGAAGGC---GGAGAAGGAAAAAAAGAAGAAGAAGGAGAAGTGGGAAGGAAGCAG
                                                                                                                                                                          GAGCACGTGGCCGAAATGTTGCGAACCATCGACTTCCAGCCGGGCGCCGCCTGGGGATGAA 1206
                                                                                                                                                                                                                                                                                    GCTCTCTACCTCCAGCAGGCAAAGGAGCTGATCAACAAGGTCGGGGGCAATGTCGAAGGTG 1086
                                                                                                                                                                                                                                                                                                                                                            TTGGAGAACGTCTCAAAGTTGGTTGAGTCAGGAATTCAGTTTATGGATGAGCCAGAAATG 1048
                                                                                                                                                                                                                                                                                                                                                                                               TTGGAGGGCTCCTCAAAGCTGGTGGAGTCCGCCATCCAGTCCATGGAGGAGCCGCAGATG 1026
                                                                                                                                                                                                                                                                                                                                                                                                                                    CGAACCCAAGAGGAGAAACTGGAACATGTCCGTGCTCTGATCAAAAAGTATTCTGATCAT 988
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGGGAGCAGGAGAAGTTGCAGCGCGTGCGGGCCTCATCCGCCAGTACGGAGACCAC 966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTCGAGACCCTGTGCGCGGTTTTGGAGGAGCGCAAGGGCGAACTGCTTCAAGCACTGGCC
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RESULT 20 AC084883 SOURCE KEYWORDS VERSION ACCESSION DEFINITION LOCUS

ACO84883 209211 bp DNA linear HTG 15-1 Mus musculus chromosome 5 clone RP23-154K6 strain C57BL6/J, AC084883 AC084883.10 HTG; HTGS_PHASE1; HTGS_DRAFT. DRAFT SEQUENCE, 21 unordered pieces. AC084883 musculus. GI:17976433

REFERENCE

ORGANISM

Mus musculus

AUTHORS Han, J., Montgomery, K.T., Grills, G., Goltz, J., Haider, A., Hall, L., Ioshi Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 209211) Ioshikhes, I.P., Chiu, D., Decker, J., Lee, E., Long, J., Murinae; Mus. Fusina, M.,

REFERENCE AUTHORS

JOURNAL TITLE

Unpublished

(bases 1 to 209211)

TITLE JOURNAL

Direct

Submission

Center: Harv

Web site:

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Center project name: ADD

Sequencing vector: pUC18; L08752
Chemistry: Dye-terminator Big Dye; 100%
*Consensus quality: 204023 at least Q20
*Consensus quality: 203326 at least Q30
*Consensus quality: 201766 at least Q40
*Stimated insert size: agarose-FP - N/A
Quality coverage: agarose-FP - N/A
Quality coverage: 10.2 x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (29-NOV-2000) Department of Molecular Genetics, Albert Einstein College of Medicine Genome Center, 1300 Morris Park Ave., Bronx, NY 10461, USA On Dec 21, 2001 this sequence version replaced g1:15148085.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Han,J., Montgomery,K.T., Grills,G., Chiu,D., Decker,J., Fusina,M., Goltz,J., Haider,A., Hall,L., Ioshikhes,I.P., Lee,E., Long,J., Pereza,A., Shim,C., Thomas,E. and Kucherlapati,R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: hpgc@mendel.mgh.harvard.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: This is a 'working draft' sequence. It currently consists of 21 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Harvard Partners Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://www.hpcgg.org/Sequence/mouse.html
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of unknown length
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of 7908
                of 85 bp in length of 1429 bp in length
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                                       61 GACAGGACTCTTCCAAGAGGGAGCAATAGCCGGGATCCCAAGAATCCAGTCAGCCTAAAC 120
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/note="assembly_name:Contig36"
119050. 133795
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147537. .161508
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76449. 99269
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30176...76428
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207862, .209211
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/note="assembly_name:Contig19"
49732 c 50169 g 53288 t
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205716. .206923
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201336. .201781
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/strain="C57BL6/J"
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                                                                                                                                                                                                                                                                                                                                                           note="assembly_name:Contig21"
                                                                                                                                                                                                                                                                                                                                                                                                                                        note="assembly_name:Contig23"
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                                                                                                                                                                                100.0%;
                                                                                                                                                                                                   25.6%;
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                                                                                                                                                              0; Mismatches
                                                                                                                                                                              Score 367; DB 2; Pred. No. 2.3e-61;
                                                                                                                                                                                                                                                                 483 others
                                                                                                                                                                                                   Length 209211;
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161509 161529 171556

Gaps

119030

30156 30176 76429 76449 99270 99270

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OM nucleic - nucleic search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Title:
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                            924.2
924.2
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12160.791 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2185239 seqs, 1125999159 residues
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SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*

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/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
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AAF27653
                       AAS42490
ABA99063
                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                                                                                                                                                         Description
                                                                Human nucleic acid
Human cytoskeleton
DNA encoding human
                         Murine muscle ring
                                              Human cDNA encodin
                                                                                                                                   Nucleotide sequenc
                                                                                                                                                      Murine muscle ring
Human protein HP03
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Nucleofine seduenc	AAF82901	22	3489	3.8	54.2	45
	2	21	3489	3.8	54.2	44
בוא ליסום	560	22	1588	3.9		43
ephila clavipes		18	2004	٠	58	42
Barr Viru	N	20	1925	4.4		41
B	AAH15376	22	1738	4.4		40
Human cDNA clone (AAH03886	22	825	4.4	ω	3 9
FLGA insert stabil	AAV55830	19	795	4.5	ω	38
splice	ABN52379	24	65	4.5	65	37
DNA clone pcek cl.	AAA59553	21	16080	4.7	66.6	ა 6
Nucleotide sequenc	AAX15650	20	10596	4.7	66.6	ω G
Plasmid pCisEBON f	AAT40348	17	10596	4.7	66.6	ω.
PC1SEBON	AAQ51731	14	10596		66.6	ω ω
en	AAZ22248	20	10380		66.6	ω N
Vector plasmid pCM	AAV21683	19	9600	4.7	66.6	ω L
Vector pshuttle DN	AAZ23778	20	8705		66.6	30
	AAX90923	20	5452		66.6	29
Epstein-Barr virus	AAI64275	24	2580	4.7	66.6	28
Nucleotide sequenc	AAA75454	21	2580		66.6	27
EBV tethering prot	AAF82902	22	1926	4.7	66.6	26
	AAA50254	21	1926	4.7	66.6	25
Nucleotide sequenc	AAV55831	19	799	4.7	66.6	24
Human regulation I	AAA98383	21	3262		70	23
Murine 7-transmemb	AAH98085	22	494	5.1	72.4	22
RFX	AAC75969	21	391	8.0	114.8	21
ORF131		21	650		161.6	20
	AAS26303	22	446		162	19
Human cDNA encodin	AAS26314	22	587		229.2	8
Human interleukin	ABN78104	24	531		267.4	17
Human ORFX ORF840	\sim	21	531	•	267.4	5
Human bone marrow	AAH89924	22	1796	•	390.6	5
Human bone marrow	90	22	1183	•	419	14
Human cDNA encodin	AAS25855	22	1762	•	439.6	<u>ا</u> ک
Murine muscle ring	ABA99062	24	2590	•	450.8	12
Human cDNA encodin	AAS25842	22	1781	33.5	478.8	_;
Human bone marrow	AAH90037	22	1231	•	480.8	10

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ALIGNMENTS

RESULT 1

WO200206318-A2. Muscle ring finger; MURF-1; mouse; cardiant; microtubule; intermediate filament; striated muscle; cardiac hypertrophy; Murine muscle ring finger protein 1 (MURF-1) coding sequence 15-JUL-2002 (first entry) ABA99061; ABA99061 standard; DNA; 1431 BP Olson EN, 18-JUL-2000; 2000US-219020P 18-JUL-2001; 2001WO-US22896. 24-JAN-2002. Mus musculus. heart disease; gene; ds. (TEXA) UNIV TEXAS SYSTEM Spencer JA; Location/Qualifiers 199..1299 /product= "MURF-1" /*tag= a

ABA83058

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention are involved in microtubule and intermediate filament stabilisation of striated muscle cells and have cardiant activity. The MURF proteins are useful for screening a candidate substance for MURF protein-binding activity, in a cell, cell-free system or in vivo, and its effect on interaction of MURF with microtubules, homodimerisation of MURF-1, MURF-2 or MURF-3 stabilisation of microtubules, interaction of MURF with intermediate filaments, e.g. desmin, vinentin and cytokeratin, and heterodimerisation of MURF. The screened compounds are useful for treating and preventing cardiac hypertrophy and heart diseases. MURF proteins are useful as antigens to immunise animals for the production of antibodies.
        601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1431 BP; 338 A; 384 C; 473 G; 236 T; 0 other;
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                                                                                                                   481
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CTGCAGCGGAACCTGCTAGTGGAGAACATCATTGACATCTACAAGCAGGAGTCCTCCCGG
                                                                                                                           CTGCAGCGGAACCTGCTAGTGGAGAACATCATTGACATCTACAAGCAGGAGTCCTCCCGG
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             GCTCGGCTTCCCGCCCCGGGAAGGTTCTCAATAAAGGACTCAAGTGTCCC 1431
                                                           ACACCCGAAGCGGAGCCAAGGGATGCTGAGGATCTGCGCAGAGAGACCACCGCGCCCAACCAC 1380
                                                                                              GAGCGGCTGGACGTGCCAGAAGGCTCAGGCCTGCACTGACCCGACTCTGATCCAGAGCGC
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                                               ACACCCGAAGCGGAGCCAAGGGATGCTGAGGATCTGCGCAGAGACCACCGCGCCCACCAA
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ARESULT 2
AAH68563
ID AAH68563;
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AC AAH68563;
XX
DT 13-SEP-2001 (first entry)
XX
XX
XX
DE Human protein HP03115 coding sequence
XX
DE Human; gene therapy; tumour; ss.
XX
PN W0200142302-A1.
XX
PN W0200142302-A1.
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PF 06-DEC-2000; 2000WO-JP08631.
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08-FEB-2000;
10-FEB-2000;
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30-MAY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is a human protein coding sequence. The human protein, preferably originated from tumour cell line, is applicable as drug, a reagent for studying intracellular protein networks and a prote source for screening proteins for binding low molecular weight drugs. Thuman protein coding sequence is useful for gene diagnosis and gene therapy, expression vectors and transformant cells for detection of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 3; Pages 236-240; 471pp; Japanese
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14-FEB-2000;
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AGGACGTTTCCGATGCCCATCTTGTAGGCACGAGGTTGTCCTGGACAGGCATGGTCTCTA
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                                         CAGGCCGCTGCACTCCAAGGCTGAGCAGCACCTCATGTGCGAGGAGCATGAAGAAGAAGAA
                                                     TGGCCTGCAGCGGAACCTGCTAGTGGAGAACATCATTGACATCTACAAGCAGGAGTCCTC
                                                                                                                                            CGTCTTCCAGGCCTCGAATCCTCTATGGCAGTCCCGGGGCTCCACCACTGTGTCTTCAGG
                                                                                                                                                                                                                                                                                                   {\tt TGCACAGCATGGACAACCTGGAGAAGCAGCTCATCTGCCCCATCTGCCTGGAGATGTT}
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99JP-0346864.

2000JP-0031062.

2000JP-0034091.

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2000JP-0035829.

2000JP-0071161.

2000JP-0160851.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 924.2; DB 22; Length 1913; Pred. No. 7.3e-197;
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                                                        Human; cardiomyopathy associated protein; CAP; myocardial biopsy; left ventricle assist device; LVAD; cardiomyopathy; ventricular tachyrhythmia; ss.
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 Location/Qualifiers 283..1359
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                                                                                                       cardiomyopathy associated protein (CAP).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acid encoding a cardiomyopathy associated protein that is differentially expressed in human left ventricle assist device (LVAD) myocardial biopsy samples, useful for diagnosing, preventing or treating cardiomyopathy
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                              CGGCCTGCAGCGAAACCTGCTAGTGGAGAACATTATCGACATTTACAAGCAGGAGTCATC
                                               TGGCCTGCAGCGGAACCTGCTAGTGGAGAACATCATTGACATCTACAAGCAGGAGTCCTC
                                                                                                           AGGACGTTTCCGATGCCCATCTTGTAGGCACGAGGTTGTCCTGGACAGGCATGGTGTCTA
                                                                                                                                                                                                                                     CTCCAAGCCCGTGGTGATCTTGCCCTGCCAACACAACCTGTGCCGCAAGTGTGCCAACGA 356
                                                                                                                                                                                                                                                                                                   TGCGCACAACATGGACAACTTGGAGAAGCAGCTCATTTGCCCCCATCTGCGAGAGATGTT
CCGGCCACTGCACGCCAAGGCTGAACAGCACCTCATGTGTGAGGAGCACGAGGACGAGAA
                                                                                           CGTCTTCCAGGCCTCGAATCCTCTATGGCAGTCCCGGGGCTCCACCACTGTGTCTTCAGG
                                                                                                                                                                         CGTCTTCCAGGCCTCTAATCCTCTGTGGCAATCCCGGGGCTCCACAACGGTGTCTTCAGG
                                                                                                                                                                                                                      CTCCAAACCAGTGGTGATCCTGCCCTGCCAACACCAGCTGTGCCGCAAATGTGCCAACGA
                                                                                                                                                                                                                                                                                  TGCACACAGCATGGACAACCTGGAGAAGCAGCTCATCTGCCCCATCTGCCTGGAGATGTT
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WW WXX DXX XXX

19-DEC-2000

AAA72433 standard;

CDNA;

1349

expressed sequence tag; drug screening; recombinant expression; reproductive disorder; infertility; immunological disorder;

Human nucleic acid-binding protein; NuABP; agonist; antagonist;

Human nucleic acid-binding protein NuABP-52 cDNA.

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                                                                                                                            GCGCACACCCGAAGCGGAGCCAAGGGATGCTGAGGATCTGCGCAGAGACCACCGCGGCA 1376
                                                                                                                                                                       GAAGAGCGGCCGGATGGGCC-----TTAAGGCCTGCGCCGACCCTGCTCGAGA
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                                                     CCCAAATCGG----CGCCGGCCCCGGGAGGATCTCAATAAAGAACTCGAGCGTCCC
                                                                                 CCAAGCTCGGCTTCCCGCCCCCGGGAAGGTTCTCAATAAAGGACTCAAGTGTCCC
                                                                                                                 GCCCGCGCTAGAGTCGGG-----
                                                                                                                                                                                        GGAGGAGCGGCTGGACGTGCCAGAAGGCTCAGGCCTGCACTGACCCGGACTCTGATCCAGA 1316
                                                                                                                                                                                                                                CGGGGAGGAAGAGGAGG-----TGGCCCCAGACGGAGAGGAGGAGGCGCGGGGCCGGA
                                                                                                                                                                                                                                                              TGGGGATGAAGAGGATGACGACATGGCTTTGGATGGGGAGGAGGGCAATGCGGGGCTGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequences AAA72382-A72436 represent cDNAs encoding novel human nucleic acid-binding proteins (NuABPs; AAB20997-B21051). These cDNAs were produced by extension from an appropriate EST (expressed sequence tag) using primers designed using the EST. The invention also relates to expression constructs, host cells and transgenic organisms comprising a human NuABP nucleic acid, recombinant production of the human NuABPs, and also to methods of and antibodies against the human NuABPs, and also to methods. The human screening modulators of human NuABP acitivity or expression. The human screening modulators of human NuABP acitivity or expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel nucleic acid binding proteins, used to identify agonists and antagonists of them, for the treatment of reproductive, immunological and cell proliferative disorders including cancer -
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P-PSDB; AAB21048.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1349 BP; 328 A; 372 C; 428 G; 221 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            arteriosclerosis, atherosclerosis, cirrhosis and psoriasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (INCY-) INCYTE PHARM INC.
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CTCCAAACCCGTGGTGATCTTGCCCTGCCAACACACCTGTGCCGAAGTGTGCCAACGA
                                                                                                                            TGCGCACAACATGGACAACTTGGAGAAGCAGCTCATTTGCCCCCATCTGCGAGATGTT
                                                                                                                                                                                                                                             GCAGGCTCCAGAGCGCCGCGGGATGAACTTCACGGTGGGTTTCAAGCCGCTGCTAGGGGA 236
                                                                                                      TGCACACAGCATGGACAACCTGGAGAAGCAGCTCATCTGCCCCATCTGCCCTGGAGATGTT
                                                                                                                                                                                                             GCACGACC-----ACCGAGGGGATGAACTTCACAGTGGGTTTCAAGCCGCTGCTAGGGGA 166
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Au-Young JL;
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88.2%;
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XX EX BX XX

30-SEP-2002

(first entry)

ABN85313 standard; cDNA; 2040

Human; cytoskeleton-associated protein; CSAP; CSAP-4;

Human cytoskeleton-associated protein, CSAP-4, coding sequence

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                                                                                                                        TGTGAGCGTGGAGCACGTGGCCGAAATGTTGCGAACCATCGACTTCCAGCCGGGCGCCGC
                                                                                                                                                                           GTCGAAGGTGGAGCTGGCAGGACGGCCGGAGCCAGGCTATGAGAGCATGGAGCAATTCTC
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Matches 1028; Conserv
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Gandhi AR, I
Gietzen KJ,
                                                                                                                                                                                                                                                                                                                                 The present sequence is the coding sequence for a human cytoskeleton associated protein (CSAP). The CSAP and its coding sequence are useful in the diagnosis, treatment and prevention of a cell proliferative disorder such as actinic keratosis, atherosclerosis, psoriasis, primary thrombocythaemia, leukaemia; a viral infection such as those caused by adenoviruses (acute respiratory disease, pneumonia), arenaviruses (lymphocytic choriomeninigitis); and a neurological disorder such as epilepsy, ischaemic cerebrovascular disease, stroke, cerebral neoplasms, Alzheimer's disease, Pick's disease, Huntington's disease or amyotrophic lateral sclerosis. The CSAP coding sequence is also useful for creating knock out or knock in humanised animals or transgenic animals to model human diseases.
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13-FEB-2001;
14-FEB-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel isolated human cytoskeleton-associated protein for diagnosing, treating or preventing atherosclerosis, psoriasis, leukemia, epilepsy, ischemic cerebrovascular disease, cerebral neoplasms and Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cell proliferative disorder; viral infection; neurological disorder;
transgenic animal; antiatherosclerotic; antipsoriatic; antiinflammatory;
virucide; anticonvulsant; vasotropic; cerebroprotective; nootropic;
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)B; ABB83475.
                                                                                                                               GCAGGCTCCAGAGCGCCGCGGGATGAACTTCACGGTGGGTTTCAAGCCGCTGCTAGGGGA
                                                                                                                                                                            ATCTAAGCGAGGAAGGGTCTACAGGCAGTGAGTGAAGGCCAGGAGCAGGGCCCAGGCCAG
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                  CTCCAAGCCCGTGGTGATCTTGCCCTGCCAACAACCTGTGCCGCAAGTGTGCCAACGA
                                                 TGCACACAGCATGGACAACCTGGAGAAGCAGCTCATCTGCCCCCATCTGCCTGGAGATGTT
                                                                TGCGCACAACATGGACAACTTGGAGAAGCAGCTCATTTGCCCCCATCTGCCCTGGAGATGTT
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Lal PG,
                                                                                                                                                                                                                                            Conservative
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; 2001US-268554P.
; 2001US-269111P.
; 2001US-271211P.
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                                                                                                                                                                                                                                                                                                        465 A; 584 C; 650 G; 341 T; 0 other;
                                                                                                                                                                                                                                                          51.3%;
78.2%;
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M, Xu Y, Walia NK,
Thangavelu K, Ison
Sanjanwala MM, Elli
                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                        Score 733.4; DB Pred. No. 3e-154;
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                                                                                                                                                                                                                                            156;
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          CCAAGCTCGGCTTCCCCGCCCCGGGAAGGTTCTCAATAAAGGACTCAAGTGTCCC
                                                                                                    GGAGGAGCGGCTGGACGTGCCAGAAGGCTCAGGCCTGCACTGACCCGACTCTGATCCAGA
                                                                                                                                     CGGGGAGGAAGAGGAGG-----TGGCCCCAGACGGAGAGGAGGGCAGCGCGGGGCCGGA
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                                                                                                                                                                               TGTGAGCGTGGAGCACGTGGCCGAAATGTTGCGAACCATCGACTTCCAGCCGGGCGCCCGC
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                                                                  GCGCACACCCGAAGCGGAGCCAAGGGATGCTGAGGATCTGCGCAGAGACCACCGCGCCA
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RESULT 6
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to human transcriptional regulator protein (TXREG) sequences. The antagonist and an agonist of the proteins of the invention are used to treat disorders associated with decreased or increased expression or activity of TXREG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated polypeptide with a human transcriptional regulator protein sequence is useful for the diagnosis, prevention and treatment of disorders associated with the immune, reproductive and cardiovascular
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                                                                                                                                                                                                                                                       GCACGACC-----ACCGAGGGGATGAACTTCACAGTGGGTTTCAAGCCGCTGCTAGGGGA
                                                                                                                                                                                                TGCACACAGCATGGACAACCTGGAGAAGCAGCTCATCTGCCCCCATCTGCCTGGAGATGTT
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                                                                                    CGTCTTCCAGGCCTCGAATCCTCTATGGCAGTCCCGGGGCTCCACCACTGTGTCTTCAGG
                                                                                                               CGTCTTCCAGGCCTCTAATCCTCTGTGGCAATCCCGGGGCTCCACAACGGTGTCTTCAGG
                                                                                                                                            CTCCAAACCAGTGGTGATCCTGCCCTGCCAACACACCTGTGCCGCAAATGTGCCAACGA
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  TGGCCTGCAGCGGAACCTGCTAGTGGAGAACATCATTGACATCTACAAGCAGGAGTCCTC
                                           AGGACGTTTCCGATGCCCATCTTGTAGGCACGAGGTTGTCCTGGACAGGCATGGTGTCTA 476
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87.5%;
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17-MAY-2000;
17-MAY-2000;
                                                                                                                                                                                                                                                                                                                                        Human; molecules for disease detection and treatment; mddt; ss; Antiarteriosclerotic; hepatotropic; antipsoriatic; cytostatic; immunosuppressive; antidiabetic; antiasthmatic; neuroprotective; osteopathic; antiarthritic; cell proliferative disorder;
                                                                                                                                                                                                                                                                                                               arteriosclerosis; cirrhosis; psoriasis; cancer; adenocarcinoma; leukaemia; breast cancer; autoimmune disorder; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                       Human cDNA encoding an mddt protein, clone LG:247384.1:2000MAY19
Panzer SR, Spiro PA, Banville SC, Shah P, Chalup MS, Cha Chen A, D'Sa SA, Amshey S, Dahl CR, Dam TC, Daniels SE, Dufour GE, Flores V, Fong WT, Greenwalt LB, Hillman JL, Liu TF, Roseberry AM, Rosen BH, Russo FD, Stockdreher TK,
                                                                                                                                                                                                                                          WO200162922-A2
                                                                                                                                                                                                                                                                                          diabetes mellitus; asthma;
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                                                               INCYTE GENOMICS INC
                                                                                                                                                                                                                                                                                        immunodeficiency syndrome; Addison's disease;
mellitus; asthma; multiple sclerosis; osteoarthritis.
                                                                                                  ; 2000US-0185213.
; 2000US-0205232.
; 2000US-0205285.
; 2000US-0205286.
; 2000US-0205287.
; 2000US-0205323.
                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                        2000US-0205324
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Chang

Jones AL; Daffo A; SC;

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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                detection and treatment (mddt proteins) and the polynucleotides encoding them. The MDDT polynucleotides and polypeptides are useful for diagnostic and therapeutic purposes e.g. to diagnose and treat cell proliferative disorders (e.g. arteriosclerosis, cirrhosis and psoriasis) cancers (e.g. adenocarcinoma, leukaemia and breast cancer) autoimmune disorders (e.g. acquired immunodeficiency syndrome (ALDS) and Addison's disease) diabetes mellitus, asthma, multiple sclerosis, osteoarthritis, and many more diseases given in the specification. The present sequence encodes an mddt protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2110 BP; 562 A; 465 C; 613 G; 470 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 121; 183pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New disease detection and treatment molecule polynucleotides and polypeptides, useful for diagnosis and treatment of arteriosclerosis, cirrhosis, psoriasis, cancer, autoimmune disorders, diabetes mellitus, asthma and multiple sclerosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to novel human molecules for disease
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                                          AAGCAACTGTTAAACCAGAGGTTCGAGACCCTGTGCGCGGTTTTGGAGGAGCGCAAGGGC 885
AAGGAAGAGCTGAGCCAGAAGTTTGACACGTTGTATGCCATCCTGGATGAGAAGAAAAGT 799
                                                                                                                                  GCAGTGATCACCCAGATGGAGGAGGTGTGCCAGACCATTGAGGACAACAGCCGCAGACAG
                                                                                                                                                                                    CAAAAGACTGAACTGAATAACTGTATCTCCATGCTGGTGGCGGGAATGACCGTGTGCAG
                                                                                                                                                                                                                                   CAGAAGAGTGAGCTGAGCGATGGCATCGCGATGCTGGTGGCGGGCAATGACCGTGTGCAG
                                                                                                                                                                                                                                                                                  AAGGTGTTTGGGATCCACAAGGCCTGCGAGGTGGCCCCATTGCAGAGTGTCTTCCAGGGA
                                                                                                                                                                                                                                                                                                                                                                             GAAGATGAGAAAATCAACATCTACTGTCTCACGTGTGAGGTGCCCCACCTGCTCCATGTGC
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                                                                                        ACCATCATCACTCAGCTGGAGGATTCCCCGTCGAGTGACCAAGGAGAACAGTCACCAGGTA
                                                                                                                                                                                                                                                                                                                    AAGGTTTTCGGCGCCCACAAGGACTGTGAGGTGGCCCCTCTGCCCACCATTTACAAACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAGGAGTGCTCCAGTCGGCCGCTGCAGAAGGGCAGT---CACCCCATGTGCAAGGAGCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches 348; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 22;
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The sequence encodes murine muscle ring finger protein 3 (MURF-3) invention relates to a purified muscle ring finger (MURF) protein

(MURF-3).

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RESULT 8
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                                 Claim 4; Page 131-133; 134pp; English.
                                                                                                                                                                                                                                                                                                                       CDS
                                                            diagnosing and treating diseases,
                                                                                                                                         Olson
                                                                      Novel muscle ring finger protein useful for
                                                                                                   P-PSDB; ABB08277.
                                                                                                                                                                 (TEXA ) UNIV TEXAS SYSTEM
                                                                                                                                                                                          18-JUL-2000; 2000US-219020P
                                                                                                                                                                                                                   18-JUL-2001; 2001WO-US22896
                                                                                                                                                                                                                                            24-JAN-2002
                                                                                                                                                                                                                                                                      WO200206318-A2
                                                                                                                                                                                                                                                                                                                                                                                  intermediate filament; s
                                                                                                                                                                                                                                                                                                                                                                                                         Muscle ring finger; MURF-3; mouse; cardiant; microtubule;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Murine muscle ring finger protein 3 (MURF-3) coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABA99063 standard;
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                                                                                                                                        Spencer JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                   Location/Qualifiers 299..1330
                                                                                                                                                                                                                                                                                             /product= "MURF-3"
                                                                                                                                                                                                                                                                                                          /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA;
                                                                                                                                                                                                                                                                                                                                                                                             striated muscle; cardiac hypertrophy;
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                                                          particularly
                                                         drug screening, and rly cardiomyopathies
                                                             for
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            stabilisation of striated muscle cells and have cardiant activity. The MURF proteins are useful for screening a candidate substance for MURF protein-binding activity, in a cell, cell-free system or in vivo, and its effect on interaction of MURF with microtubules, homodimerisation of MURF, MURF-1, MURF-2 or MURF-3 stabilisation of microtubules, interaction of MURF with intermediate filaments, e.g. desmin, vimentin and cytokeratin, and heterodimerisation of MURF. The screened compounds are useful for treating and preventing cardiac hypertrophy and heart diseases. MURF proteins are useful as antigens to immunise animals for the production of antibodies.
1006
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Pred. No. 1e-98;
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Query Match Best Local Similarity

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                             The present sequence is the coding sequence for a human transcription factor. The transcription factor and its coding sequence are useful in the diagnosis, treatment and prevention of diseases associated with altered expression of the transcription factor e.g. cell proliferative, autoimmune/inflammatory, neurological and developmental disorders. A number of specific disorders/diseases are given in the specification, including: arteriosclerosis, cirrhosis, hepatitis, cancers, AIDS, allergies, anaemia, asthma, autoimmune thyroiditis, bronchitis, atopic dermatitis, diabetes mellitus, emphysema, Goodpasture's syndrome, gout, Grave's disease, multiple sclerosis, osteoarthritis, pancreatitis, psoriasis, rheumatoid arthritis, systemic lupus erythematosus, ulcerative colitis, uveitis, Alzheimer's disease, Huntington's disease, Parkinson's disease, stroke, and viral, bacterial, fungal and protozoal infections.
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 Sequence 1764 BP; 473 A; 399 C; 516 G; 376 T; 0 other;
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                                  GCGGGGCTGGAGGAGGAGCGGCTGGCCAGAAGG 1283
                                                                   ACAGATGAGGAAGAAGAATTCATTGAAGAAGAAGATCAGGAAGAGGAAGAGTCCACA 1157
                                                                                                     CCGGGCGCCGCTGGGGATGAAGAGGATGACGACATGGCTTTGGATGGGGAGGAGGAAT 1245
                                                                                                                                            GACTTCTTTACTTTGGATTTAGAGCACATAGCAGACGCCCTGAGAGCCATTGACTTTGGG
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AAH90037
                                                             Matches
                                                                         Query Match
Best Local
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                                                                                                                                                     be genetic, may be caused by a viral (e.g. HIV), bacterial or fungal infection, or may result from an autoimmune disorder, a coagulation disorder (e.g. haemophilia), inhibition of tumour cell proliferation, suppression of an inflammatory response or treatment of a nervous system disorder such as Alzheimer's disease. Detection of the presence or increased expression of the polynucleotide or the protein it encodes is useful for the diagnosis and/or prognosis of one or more types of cancer. The polynucleotide and polypeptide can be used as nutritional sources or supplements and in the screening of
                                                                                                                                                                                                                                                                                     expressed in the bone marrow. The polynucleotide and the polypeptide encoded by it are useful in the treatment of various immune deficiencies and disorders. The deficiencies and disorders may
                                                                                                                 Sequence 1231 BP; 332 A; 305 C;
                                                                                                                                             chemical compounds as potential drugs.
                                                                                                                                                                                                                                                                                                                               The present sequence is one of 251 novel human polynucleotides
                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 397; 648pp; English
                                                                                                                                                                                                                                                                                                                                                                                       Novel bone-marrow-expressed polynucleotides and polypeptides, for treating e.g. cancer and immune deficiency disorders -
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03-AUG-2000;
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25-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; bone marrow; antiinflammatory; cytostatic; neuroprotective; antiviral; antibacterial; antifungal; anti-HIV; haemostatic; immunosuppressive; gene therapy; cytokine cell proliferation; cell differentiation modulator; immune disorder; infection; cancer; human immunodeficiency virus; HIV; autoimmune disorder; haemophilia;
              226 CTGCTAGGGGATGCGCACAACATGGACAACTTGGAGAAGCAGCTCATTTGCCCCCATCTGC 285
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19-OCT-2000;
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TGATCCAGGATGGGAATCCCATGGAGAACTTGGAGAAGCAGCTGATCTGCCCTATCTGC
                                                           696;
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                                                                         Similarity
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Zhou P,
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                                                           Conservative
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2000US-0693036.
2000US-0250583.
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2000US-0620312.
2000US-0653450.
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                                                                    33.6%;
                                                          0;
                                                        Score 480.8; DB 2
Pred. No. 6.9e-98;
D; Mismatches 337
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                                                                                                                  361 G;
                                                                                                                 233 T;
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                                                          337;
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                                                                                                             GACTTCTTTACTTTGGATTTAGAGCACATAGCAGACGCCCTGAGAGCCATTGACTTTGGG
                                                                                                                              GAGCAATTCTCTGTGAGCGTGGAGCACGTGGCCGAAATGTTGCGAACCATCGACTTCCAG
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GAAGGGAAGGAAG
                           GCGGGGCTGGAGGAGG 1261
                                                       ACAGATGAGGAAGAAGAATTCATTGAAGAAGAAGATCAGGAAGAGGAAGAGTCCACA
                                                                               CCGGGCGCCGCTGGGGATGAAGAGGATGACGACATGGCTTTGGATGGGGAGGAGGGCAAT
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RESULT 11 AAS25842 ID AAS2

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14-AUG-2000
12-AUG-2000
22-AUG-2000
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22-AUG-2000
23-AUG-2000
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20-SEP-2000
01-SEP-2000
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26-JUL-2000;
26-JUL-2000;
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11-JUL-2000;
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28-JUN-2000;
30-JUN-2000;
07-JUL-2000;
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04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cerebrovascular disorder; cerebral ischaemia; angiogenesis nervous system disorder; Alzheimer's disease; infection; oc corneal infection; wound healing; epithelial cell prolifera
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19-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; opthalmalogical; vulnerary; secreted protein; rheumatoid arthritis; hyperproliferative disorder; cardiovascular disorder; cardiac arrest;
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14-AUG-2000;
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17-MAR-2000;
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2000US-0229287.
2000US-0229343.
2000US-0229345.
2000US-0229545.
2000US-0229509.
2000US-0229509.
2000US-0230437.
2000US-0231243.
2000US-0231243.
2000US-0231243.
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2000US-0209467
2000US-0209467
2000US-0214886
2000US-0216647
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2000US-0217496
2000US-0217496
2000US-021963
2000US-022964
2000US-022964
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DB; AAU15855.
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Claim 1; SEQ ID No 21; 980pp; English.
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New nucleic acid molecules encoding 461 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions used as food additives or preservatives and

The invention relates to isolated nucleic acid molecules and their CC encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, CC rabbits, goats, horses, cats, dogs, chickens or sheep. They CC are also used in diagnosing a pathological condition or susceptibility CC to a pathological condition. Antibodies to the proteins can also CC diagnostic immunoassays e.g. radioimmunoassays or enzyme linked CC include autoimmune diseases e.g. rheumatoid arthritis, CC hyperproliferative disorders e.g. cardiac arrest, cerebrovascular disorders (CC ardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, very system disorders e.g. cardiac arrest, very system disorders (CC and occular disorders e.g. corneal infection, and many other CC disorders listed in the specification. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to CC be used to aid wound healing and epithelial cell proliferation, to cregenerate tissues and in chemotaxis. The polypeptides can also be used to aid wound in chemotaxis. The polypeptides can also be used to aid wound healing cell culture of primary tissues, to cregenerate tissues and in chemotaxis. The polypeptides can also be used to said forcers and other nutritional components. The present of capabilities, fat content, lipid, protein, carbohydrate, vitamins, combaning confectors and other nutritional components. The present sequence encodes a novel secreted protein of the invention.

317 TCCATGTCTGGAGGCCGTTTCCGCTGCCCCACCTGCCGCCACGAGGTGATCATGGATCGT GTGTCTTCAGGAGGACGTTTCCGATGCCCATCTTGTAGGCACGAGGTTGTCCTGGACAGG TGTGCCAATGACATCTTCCAGGCTGCAAATCCCTACTGGACCAGCCGGGCAGCTCAGTG TGTGCCAACGACGTCTTCCAGGCCTCTAATCCTCTGTGGCAATCCCGGGGGCTCCACAACG CTGATCCAGGATGGGAATCCCATGGAGAACTTGGAGAAGCAGCTGATCTGCCCTATCTGC CTGCTAGGGGATGCGCACAACATGGACAACTTGGAGAAGCAGCTCATTTGCCCCATCTGC 0; Score 478.8; DB 22 Pred. No. 2.1e-97; 0; Mismatches 352; Indels 3; Gaps 465 316 405 345 196 256 1;

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Mus musculus
                                                      Muscle ring finger; MURF-2; mouse; cardiant; microtubule;
                                                                                 Murine muscle ring finger protein 2 (MURF-2) coding sequence
                                                                                                                  15-JUL-2002
                                                                                                                                                                            ABA99062 standard;
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                                         intermediate filament;
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                          gene;
                           ds.
                                         striated muscle; cardiac
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Key
CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2590 BP; 703 A; 627 C; 625 G; 635 T; 0 other;
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               CACGCCAAGGCTGAACAGCACCTCATGTGTGAGGAGCACGAGGACGAGAAGATCAACATC
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                                              AGGAACCTGCTCGTGGAAAACATTATTGATATCTACAAGCAGGAATCCACCAGGCCAGAA
                                                                                CGGAACCTGCTAGTGGAGAACATCATTGACATCTACAAGCAGGAGTCCTCCCGGCCACTG 546
                                                                                                                CGATGCCCATCTTGTAGGCACGAGGTTGTCCTGGACAGGCATGGTGTCTATGGCCTGCAG
                                                                                                                                                                                 GCCTCTAACCCGTACTTACCCACAAGAGGAGGCACCACCGTGGCATCAGGGGGGCCGCTTC
                                                                                                                                                                                                                                                GTGGTCATTCTCCCTTGCCAGCACCACCTGTGCAGGAAATGTGCCAGTGACATCTTCCAG
                                                                                                                                                                                                                                                                                 GTGGTGATCTTGCCCTGCCAACACAACCTGTGCCGCAAGTGTGCCAACGACGTCTTCCAG
                                                                                                                                                                                                                                                                                                                ATGGATAACTTGGAAAAGCAACTGATCTGTCCCATCTGCCTAGAGATGTTCACGAAGCCT 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to immunise animals for the production of antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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/product= "MURF-2"
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Score 450.8; 1
Pred. No. 4.2e
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RESULT 13
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XX AAS25
XX AAS25
XX O7-NC
DT 07-NC
XX Human
XX Human
KW Cytos
KW reurc
KW reurc
KW recreb
KW hyper
KW hyper
KW hyper
KW hyper
KW hyper
KW hyper
KW ocereb
KW nervo
XX Skin
XX
                                   Human; immunosuppressive; antiarthritic; ss; antirheumatic; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; opthalmalogical; vulnerary; secreted protein; rheumatoid arthritis; hyperproliferative disorder; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; cerebral ischaemia; angiogenesis; nervous system disorder; Alzheimer's disease; infection; ocular disorder; corneal infection; wound healing; epithelial cell proliferation; skin ageing; food additive; preservative; antiproliferative.
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                                                                                                                                                                      Human cDNA encoding a novel secreted protein, Seq ID 34.
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            sapiens
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 14-SEP-2000;
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26-JUL-2000;
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28-JUN-2000;
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SC,
Ruben SM
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Matches Query Match Best Local

Local Sir hes 703;

Similarity

Conservative

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Score 439.6; Pred. No. 1.2e-88 Mismatches 374;

DB 22;

Length 1762;

Indels

9;

Gaps

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The invention relates to isolated nucleic acid molecules and their CC encoded secreted proteins. The nucleic acids and proteins are used to grevent, treat or ameliorate a medical condition in e.g. humans, mice, CC rabbits, goats, horses, cats, dogs, chickens or sheep. They care also used in diagnosing a pathological condition or susceptibility CC to a pathological condition. Antibodies to the proteins can also CC diagnostic immunoassays e.g. radioimmunoassays or enzyme linked CC immunosorbant assays (ELISA). Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, CC cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cand ocular disorders e.g. conneal infection, and many other CC and ocular disorders e.g. corneal infection, and many other CC disorders listed in the specification. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to CC prevent skin aging due to sunburn, to maintain organs before CC transplantation, for supporting cell culture of primary tissues, to as a food additive or preservative to increase or decrease storage CC canabilities. fat content, linid, mortein, carbohydrate, vitamins cCC carbohydrate, intermine CCC carbohydrate.
                                                                                                      capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional components. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid molecules encoding 461 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and
                                                                                 sequence encodes a novel secreted protein of the invention.
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P-PSDB; AAU15868.
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30.7%;
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Qy Дb Qy 뫄 Qy DЪ Qy Дb δÃ В δÃ DЬ Qy В Qy 145 325 666 GGACTGTGAGGTGGCCCCTCTGCCCACCATTTACAAACGCCAGAAGAGTGAGCTGAGCGA 486 385 426 265 187 GAGCGCCGCGGGATGAACTTCACGGTGGGTTTCAAGCCGCTGCTAGGGGGATGCGCACAAC CTACTGTCTGAACTGCGAAGTACCCACCTGCTCTCTGTGCAAGGTGTTTGGTGCACACAA CTACTGCCTGAGCTGCGAGGTGCCCACCTGCTCTCTCTGCAAGGTTTTCGGCGCCCACAA GCGGAACCTGCTAGTGGAGAACATCATTGACATCTACAAGCAGGAGTCCTCCCGGCCACT CCGATGCCCATCTTGTAGGCACGAGGTTGTCCTGGACAGGCATGGTGTCTATGGCCCTGCA GGCCTCTAACCCGTATTTGCCCCACAAGAGGAGGTACCACCATGGCATCAGGGGGGCCGATT GGCCTCTAATCCTCTGTGGCAATCCCGGGGCTCCACAACGGTGTCTTCAGGAGGACGTTT GTGGTAGATTCTCCCTTGTCAGCACCACCTGTGTAGGAAATGTGCCCAGTGATATTTTCCA GTGGT-GATCTTGCCCTGCCAACACACCTGTGCCGCAAGTGTGCCCAACGACGTCTTCCA GACAGCGAGGAGGATGAGCGCATCTCTGAATTACAAATCTTTTTCCAAAGAGCAGCAGACC GCACGCCAAGGCTGAACAGCACCTCATGTGTGAGGAGCACGAGGACGAGAAGATCAACAT GAGGAACCTGCTGGTGGAAAATATCATTGACATCTACAAGCAGGAGTCCACCAGGCCA--CCGCTGCCCATCCTGTAGACATGAAGTGGTTTTTGGATAGACATGGGGTATATGGACTTCA ATGGACAACTTGGAGAAGCAGCTCATTTGCCCCATCTGCCTGGAGATGTTCTCCAAGCCC ----GAAAAGAAATCCGACCAGCCCATGTGCGAGGAACATGAAGAGGAGCGCATCAACAT _____ 384 365 264 246

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ford JE, Boyle BJ, Ren F, Wang J, We Zhao QA, Zhou P, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1183 BP; 294 A; 318 C; 327 G; 244 T; 0 other;
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30-NOV-2000; 2000US-0250583.
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           CAGAAGAGTGAGCTGAGCGATGGCATCGCGATGCTGGTGGCGGGCAATGACCGTGTGCAG
                                                                                                                                              2001-488707/53.
DB; AAM00998.
CAAAAGACTGAACTGAATAACTGTATCTCCATGCTGGTGGCGGGGAATGACCGTGTGCAG
                                                              AAGGTGTTTTGGGATCCACAAGGCCTGCGAGGTGGCCCCATTGCAGAGTGTCTTCCAGGGA
                                                                              AAGGTTTTCGGCGCCCACAAGGACTGTGAGGTGGCCCCTCTGCCCACCATTTACAAACGC
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Werhman T, Xu
, Drmanac RT;
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Pred. No. 4.4e-84;
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Yang Y, Zhar
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09-JUL-2000;
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19-OCT-2000;
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             Claim 1;
                                  Novel bone-marrow-expressed polynucleotides and polypeptides, useful for treating e.g. cancer and immune deficiency disorders \mbox{-}
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                                                                                                                                                                                                                                                                                                                                                                                                          immunodeficiency virus; HIV; autoimmune disorder; haemophilia;
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                                                                                                                                                                HYSEQ INC.
             Page 243-244;
                                                                                                             ang J, W
Zhou P,
                                                                                                                                      Boyle BJ,
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2000US-0598042.
2000US-0620312.
2000US-0653450.
2000US-0662191.
2000US-0693036.
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Werhman T, Xu
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             648pp; English
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KuC, Xue
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is one of 251 novel human polynucleotides expressed in the bone marrow. The polynucleotide and the polypeptide encoded by it are useful in the treatment of various polypeptide encoded by it are useful in the treatment of various polypeptide.
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TCATCCAGCAGTACCAGGAGCAGCTGGACAAGTCCACAAGCTGGTGGAAACTGCCATCC
                                                                                                                GCGAACTGCTTCAAGCACTGGCCCGGGAGCAGGAGGAGAAGTTGCAGCGCGTGCGGGGCC
                                                                                                                                                                                                                                                                                                                 ACAAAAGACTGAACTGAATAACTGTATCTCCATGCTGGTGGCGGGGAATGACCGTGTGCA
                                    TCATCCGCCAGTACGGAGACCACTTGGAGGGCTCCTCAAAGCTGGTGGAGTCCGCCATCC
                                                                             GTGAGTTGCTGCTGCGGATCTCGCAAGAGCAGGAAAAGAAGCTTATCTTCATCGAGGCCC
                                                                                                                                                           <u>AAATAGAAGAGCTGAGCCAGAAGTTTGACACGTTGTATGCCCATCCTGGATGAAAAGAAAA</u>
                                                                                                                                                                                              AGAAGCAACTGTTAAACCAGAGGTTCGAGACCCTGTGCGCGGTTTTGGAGGAGCGCAAGG
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RESULT 16
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02-APR-1999;
05-APR-1999;
30-MAR-2000;
                                                                   Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
       AAC74446 to
                                       Claim 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant, immunosuppressant; cardiant, immunosuppressant; cardiant, immunosuppressive; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; hypotensive; dermatological; inmunosuppressive; antiinflammatory; antitiviral; antibacterial; antifungal; antifinematic; antithyroid; antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; hone demandary; and allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
                                                                                                                                                                                                   Shimkets RA, Leach M;
                                                                                                                                                                                                                                       (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                31-MAR-2000; 2000WO-US08621.
                                                                                                                                                                                                                                                                                                                                                                                                   05-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          thrombosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human ORFX ORF840 polynucleotide sequence SEQ ID NO:1679.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAC75285 standard; cDNA; 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1184 AGCCGGGCGCCGCTGGGGATGAAGAGGATGACGACATGGCTTTGGATGGGGAGGAGGGCA 1243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            damage;
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                                                                                                                                               AAB41076.
                                   Page 1334; 5507pp; English.
   AAC77606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          contraceptive;
                                                                                                                                                                                                                                                                      2000US-0540763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cartilage damage; antiinflammatory disease; coagulation;
                                                                                                                                                                                                                                                                                     99US-0127607.
99US-0127636.
99US-0127728.
encode the proteins
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                                                                     Human interleukin receptor-like ORF3051 cDNA, SEQ ID NO:6101.
                                                                                                                   08-JUL-2002
                                                                                                                                                          ABN78104;
                                                                                                                                                                                              ABN78104 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an OREX-associated disorder. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 531 BP; 129 A; 143 C; 150 G; 108 T; 1 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           262 TCCATGTCTGGAGGCCGTTTCCGCTGCCCTACCTGCCGCCACGAGGTGATCATGGATCGT
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                                                                                                                                                                                                                                                                                                                                      AAGGTTTTCGGCGCCCACAAGGACTGTGAGGTG 678
                                                                                                                                                                                                                                                                                                                                                                          GAAGATGAGAAAATCAACATCTACTGTCTCACGTGTGAGGTGCCCACCTGCTCCATGTGC
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                                                                                                                                                                                                531 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 267.4; DB 21; Length 531; Pred. No. 2.6e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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Human; ORF; open reading frame; ORFX; drug screening; diagnosis; disease monitoring; cytokine; cell proliferation; cell differentiation;

immune modulation; haematopoiesis regulation; tissue

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angiogenesis; activin; inhibin; chemotactic; chemokinetic; haemostatic; thrombolytic; tumour inhibition; bodily characteristic; fertility; behaviour; cancer; proliferative disorder; neurological disorder; cardiovascular disease; immune system disorder; organ transplantation; tissue growth disorder; tissue regeneration disorder; diabetes mellitus; vasotropic; antipsoriatic; antidiabetic; cytostatic; nootropic; vasotropic; antipsoriatic; antidiabetic; cytostatic; nootropic; cardiant; hypotensive; antithyroid; antilfalmmatory; immunomodulator; cardiant; hypotensive; antithyroid; antitharmatory; immunomodulator; dermatological; analgesic; virucide; antibacterial; fungicide; gene; ss.
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Homo sapiens

WO200190366-A2

29-NOV-2001.

24-MAY-2001; 2001WO-US17076

24-MAY-2000; 2000US-206690P

(CURA-) CURAGEN CORP

Leach MD, Shimkets RA;

Ω

Qy В δõ Вþ Qy 밁 δÃ. Б

없

WPI; 2002-106200/14. ABP34078

Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and disorders related to organ transplantation

Claim 1; Page 1775; 2508pp; English.

Compared to the control of the invention activity. Compared and entioning frame) 1-4534, and sequences ABM75054-CC ABM75057 represent cDNAs encoding them. The invention also encompasses complypeptides at least 80% identical to the ORFI ORFA534 (collectively creferred to as ORFX) proteins, polynucleotides at least 85% identical to the ORFI ORFA534 (collectively creferred to as ORFX) proteins, polynucleotides at least 85% identical to the ORFI ORFA534 (collectively creferred to as ORFX) proteins, polynucleotides at least 85% identical to comprising ORFX proteins, antibodies compression or continuous control of ORFX proteins, antibodies specific for ORFX proteins, methods of detecting ORFX proteins, antibodies comprising ORFX proteins, antibodies of compared proteins of the invention have a wide creativity, and methods of screening individuals for a predisposition to an ORFX associated disorder. The ORFX proteins of the invention have a wide crange of biological activities, such as cytokine, cell proliferation, cell differentiation, immune modulation, haematopoiesis regulation, cell individuals creativity, chemotactic/cell differentiation, immune modulation, haematopoiesis regulation, cell proliferation, cell differentiation, immune modulation, haematopoiesis regulation, cell cell differentiation, immune modulation, haematopoiesis regulation, cell proliferation, cell differentiation, immune asystem disorders proteins, cell to be involved in the determination of bodily characteristics, fertility and behaviour. ORFX proteins, cell to calce and antibodies may be used in the treatment of cancers, concluded and antibodies may be used in the treatment of cancers, concluded and antibodies may be used in the treatment of cancers, concluded and infectious diseases caused by viral, bacterial, cell diseases, in municipally be used to or transcripts, in the detection and cloning of homologous concluded in a disorder and collection of ORFX personal call minustry of ORFX nucleic acids may also be used as a source of proteins an which may be useful for studying the function and/or activity of ORFX protein, and in drug screening. The ORFX proteins may also be used as immunogens to generate specific antibodies, which are useful in the diagnosis, treatment and monitoring of ORFX-associated diseases

531 129 A; 143 C; 150 G; 108 T; 1 other;

Score 267.4; DΒ Length 531;

Query Match

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Best Local Similarity 75.9
Matches 344; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     226 CTGCTAGGGGATGCGCACAACATGGACAACTTGGAGAAGCAGCTCATTTGCCCCATCTGC
                                                                                                     439
                                                                                                                                                                                                             382
                                                                                                                                                                                                                                                                                                                     322
499 AAGGTGTTTGGGATCCACAAGGCCTGCGAGGTG 531
                                                                                                                                                                                                                                                                                                                                                                   466 CATGGTGTCTATGGCCTGCAGCGGAACCTGCTAGTGGAGAACATCATTGACATCTACAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82 CTGATCCAGGATGGGAATCCCATGGAGAACTTGGAGAAGCAGCTGATCTGCCCTATCTGC 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGTGCCAACGACGTCTTCCAGGCCTCTAATCCTCTGTGGCAATCCCGGGGGCTCCACAACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGGAGATGTTCTCCAAGCCCGTGGTGATCTTGCCCTGCCAACACAACCTGTGCCGCAAG 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTGGAGATGTTTACCAAGCCAGTGGTCATCTTGCCGTGCCAGCACAACCTGTGCCGGAAG
                                                 AAGGTTTTCGGCGCCCACAAGGACTGTGAGGTG 678
                                                                                                     GAAGATGAGAAAATCAACATCTACTGTCTCACGTGTGAGGTGCCCACCTGCTCCATGTGC
                                                                                                                                   GAGGACGAGAAGATCAACATCTACTGCCTGAGCTGCGAGGTGCCCACCTGCTCTCTGC
                                                                                                                                                                                                             CAGGAGTGCTCCAGTCGGCCGCTGCAGAAG---
                                                                                                                                                                                                                                                              CAGGAGTCCTCCCGGCCACTGCACGCCAAGGCTGAACAGCACCTCATGTGTGAGGAGCAC
                                                                                                                                                                                                                                                                                                               CACGGAGTGTACGGCCTGCAGAGGAACCTGCTGGTGGAGAACATCATCGACATCTACAAA
                                                                                                                                                                                                                                                                                                                                                                                                                       TCCATGTCTGGAGGCCGTTTCCGCTGCCCTACCTGCCGCCACGAGGTGATCATGGATCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTGTCTTCAGGAGGACGTTTCCGATGCCCATCTTGTAGGCACGAGGTTGTCCTGGACAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGTGCCAATGACATCTTCCAGGCTGCAAATCCCTACTGGACCAGCCGGGGCAGCTCAGTG
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                                                                                                                                                                                                             GGCAGTCACCCCATGTACAAGGAGCAC
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RESULT 18 AAS26314 07-NOV-2001 AAS26314 standard; cDNA; (first entry) 587

밁 Ş 당 δÃ ₽

Human cDNA encoding a novel secreted protein, Seg ID

vulnerary; secreted protein; rheumatoid arthritis; hyperproliferative disorder; cardiovascular disorder; cardiovascular disorder; cerebrovascular disorder; cerebral ischaemia; angiogenesis; nervous system disorder; Alzheimer's disease; infection; ocular disorder; corneal infection; wound healing; epithelial cell proliferation; neuroprotective; antibacterial; virucide; fungicide; Human; immunosuppressive; antiarthritic; ss; antirheumatic; cytostatic; cardiant; vasotropic; cerebroprotective; ageing; food additive; preservative; antiproliferative nootropic; opthalmalogical;

Ното

WO200155322-A2

ACC CARREST CONTRACTOR 02-AUG-2001

17-JAN-2001; 2001WO-US01341

04-FEB-2000; 24-FEB-2000; 02-MAR-2000; 16-MAR-2000; 31-JAN-2000; 2000US-0179065. 2000US-0180628. 2000US-0184664. 2000US-0186350. 2000US-019874. 2000US-0198123. 2000US-0198123. 2000US-0205515. 2000US-0209467.

17-MAR-2000;

18-APR-2000; 19-MAY-2000;

28-JUN-2000; 30-JUN-2000; 07-JUL-2000; 07-JUL-2000;

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20-OCT-2000)
20-OCT-2000)
20-OCT-2000)
20-OCT-2000)
20-OCT-2000)
01-NOV-2000)
08-NOV-2000)
17-NOV-2000)
The invention relates to isolated nucleic acid molecules and their encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility
                                                                                                                                   New nucleic acid molecules encoding 461 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions used as food additives or preservatives -
                                                                                                          Claim
                                                                                                                                                                                                                P-PSDB;
                                                                                                                                                                                                                                                                                                (HUMA-)
                                                                                                                                                                                                                                2001-488783/53.
                                                                                                                                                                                                                AAU16327.
                                                                                                                                                                                                                                                                                                HUMAN GENOME
                                                                                                          SEQ ID No
                                                                                                                                                                                                                                                                  Barash
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2000US-0241809.
2000US-024181809.
2000US-0246477.
2000US-0246477.
2000US-0246477.
2000US-0246477.
2000US-0246477.
2000US-0246477.
2000US-0246525.
2000US-0246526.
2000US-0246527.
2000US-0246528.
2000US-0246528.
2000US-0246610.
2000US-0246610.
2000US-0246611.
2000US-0246611.
2000US-0249207.
2000US-0249217.
2000US-0249217.
2000US-0249217.
2000US-0249217.
2000US-0249217.
2000US-0249218.
2000US-0251186.
2000US-0251186.
2000US-0251198.
2000US-0251198.
2000US-0251198.
2000US-0251198.
2000US-0251198.
2000US-0251198.
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                                                                                                   493; 980pp; English.
                                                                                                                                                                                                                                                                                                  SCI INC
                                                                                                                                                                                                                                                                  Ruben
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2000US-0214886.
2000US-0215419.
2000US-0216880.
2000US-0217486.
2000US-0217486.
2000US-0217486.
2000US-0218290.
2000US-0224518.
2000US-0224518.
2000US-0225266.
2000US-0225266.
2000US-0225277.
2000US-0225277.
2000US-0225277.
2000US-0225277.
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2000US-0225277.
2000US-0225279.
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2000US-0225279.
2000US-0225279.
2000US-0225279.
2000US-0229343.
2000US-0229343.
2000US-0239363.
2000US-0231244.
2000US-0231414.
2000US-0231414

14-AUG-2000 12-AUG-2000 12-AUG-2000 12-AUG-2000 13-AUG-2000 13-AUG-2000 10-SEP-2000 10-SEP-2000 10-SEP-2000 10-SEP-2000 10-SEP-2000 10-SEP-2000 10-SEP-2000 11-SEP-2000 11-CCT-2000 11-CCT-2000 21-SEP-2000 21-CCT-2000 21-CCT-2000 21-CCT-2000 21-CCT-2000 21-CCT-2000 21-CCT-2000 21-CCT-2000

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RESULT 19
AAS26303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to a pathological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in CC diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunosorbant assays (ELISA). Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis. CC impurosorbant assays (ELISA). Disorders which are diagnosed or treated conclude autoimmune diseases e.g. rheumatoid arthritis. CC include autoimmune diseases e.g. rheumatoid arthritis. CC reprovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, viruses and funging and ocular disorders e.g. corneal infection, and many other considered in the specification. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to compenent skin aging due to sumburn, to maintain organs before cransplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional components. The present cc sequence encodes a novel secreted protein of the invention.
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                      cytostatic; cardiant; vasotropic; cerebroprotective; nootropic;
neuroprotective; antibacterial; virucide; fungicide; opthalmalogical;
                                                                                                                       Human; immunosuppressive; antiarthritic; ss; antirheumatic;
                                                                                                                                                                                                                                 07-NOV-2001
                                                                                                                                                                                                                                                                                  AAS26303;
                                                                                                                                                                                                                                                                                                                                     AAS26303 standard;
                   vulnerary; secreted protein; rheumatoid arthritis; hyperproliferative disorder; cardiovascular disord
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  538
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GACAGCGAGGAGATRAGCGCATCTCTGAATTACAAATCTTTTTCCAAAGAGCAGCAGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TACTGTCTGAACTGCGA-ATACCCACCTGCTCTGTGCAAGGTGTTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCCTCTAATCCTCTGTGGCAATCCCGGGGCTCCACAACGGTGTCTTCAGGAGGACGTTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CACGCCAAGGCTGAACAGCACCTCATGTGTGAGGAGCACGAGGAGGAGGAGAGATCAACATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TACTGCCTGAGCTGCGAGGTGCCCACCTGCTCTCTCTGCAAGGTTTTCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---GAAAAGAAATCCGACCAGCCCATGTGCGAGGAACATGAAGAGGAGCGCATCAACATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      333;
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Similarity 70.9%;
                                                                                                                                                                           encoding a novel secreted protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                     cDNA; 446
cerebral
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 229.2;
Pred. No. 9e-
                                                                                                                                                                                                                                                                                                                                     ВP
                     cardiovascular disorder; cardiac arrest;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9e-42;
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angiogenesis
                                                                                                                                                                           Seq ID
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δÃ 밁 Ş В Qy 밁 Ωy 밁 δÃ

δÃ В δÃ Ъ Š Вþ

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08-SEP-2000;
12-SEP-2000;
14-SEP-2000;
14-SEP-2000;
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18-AUG-2000;
22-AUG-2000;
22-AUG-2000;
23-AUG-2000;
30-AUG-2000;
01-SEP-2000;
01-SEP-2000;
01-SEP-2000;
01-SEP-2000;
01-SEP-2000;
01-SEP-2000;
05-SEP-2000;
05-SEP-2000;
06-SEP-2000;
06-SEP-2000;
08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
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14-AUG-2000;
14-AUG-2000;
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14-AUG-2000;
14-AUG-2000;
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14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nervous system disorder; Alzheimer's disease; infection; ocular disorder; corneal infection; wound healing; epithelial cell proliferation; skin ageing; food additive; preservative; antiproliferative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-MAR-2000;
16-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                            07-JUL-2000;
11-JUL-2000;
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18-APR-2000;
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438
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P-PSDB; AAU16316.
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05-JAN-2001; 2001US-0259678.
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RESULT 20
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ID AAC75

AAC75760 standard; cDNA; 650

AAC75760;

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antiviral; antibacterial; antifungal; antirheumatic; antithyroid; antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
                                                                                                                                                                              immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidlabetic; hypotensive; dermatological; immunosuppressive; antihinflammatory; antibacterial; antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus,
                                                                                                                                                                                                                                                                                                                                                                                                       AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames I to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-MAR-1999; 99US-0127607.
05-APR-1999; 99US-0127636.
05-APR-1999; 99US-0127728.
30-MAR-2000; 2000US-0540763.
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                                                               hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel nucleic acids and peptides derived from open reading frame useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
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                                            coagulation;
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                                               inhibit thrombosis; and as a contraceptive.
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Query Match

Sequence 650 BP; 171 A; 150 C; 212 G; 116 T; 1 other;

11.38;

Score 161.6;

DB 21; Length 650;

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               TGGTGATCTTGCCCTGCCAACACCTGTGCCGCAAGTGTGCCAACGACGTCTTCCAGG
                                                                        TGGACAACTTGGAGAAGCAGCTCATTTGCCCCCATCTGCAGATGTTCTCCCAAGCCCG 307
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                                                                                                                                               AGCGCCGCGGGATGAACTTCACGGTGGGTTTCAAGCCGCTGCTAGGGGGATGCGCACAACA 247
TGGTGATCCTGCCTGCCAACACCTGTGCCGCAAATGTGCCAACGACGTCTTCCAGG
                                                           TGGACAACCTGGAGAAGCAGCTCATCTGCCCCATCTGCCTGGAGATGTTCTCCAAACCAG
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0; Mismatches 29;
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5: /ggn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/Dackfiles1.seq:*
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                                                                                                                                                                                                                                                                                                                                                                               Match Length
                                                                                                                                                                                                                                                                                                                                                                                          Query
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                                            21442421245211114424
             US-09-484-970B-37
US-09-561-989-9
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US-09-56-863-2
US-09-359-863-2
US-09-310-141-1
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US-08-28-328-11
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7314.241 Million cell updates/sec
Sequence 37, Appli Sequence 2, Appli Sequence 2, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 15, Appl Sequence 17, Appli Sequence 17, Appli Sequence 17, Appli Sequence 18, Appli Sequence 17, Appli Sequence 17, Appli Sequence 17, Appli Sequence 20, Appli Sequence 21, Appli Sequence 1, Appli
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406 GTGTCTTCAGGAGGACGATTCCCGATGCCCATCTTGTAGGCACGAGGTTGTCC	226 CTGCTAGGGGATGCCACAACATGACAACTTGGACAAGCAG 226 CTGCTAGGGGATGCCACAACATGGACAACTTGGACAAGCAG 211	1.1 1.484-970B-37	45.6 3.2 1505 1 US-07-915-246-1 45.6 3.2 331 3 US-08-864-038A-2 145.6 3.2 3331 3 US-08-864-038A-4 145.6 3.2 351 1 US-08-964-038A-4 145.6 3.2 9551 1 US-08-966-200-93 145.6 3.2 9551 2 US-08-96-200-93 145.6 3.1 1995 1 US-08-425-069-3 144.6 3.1 1995 2 US-08-317-944B-3 144.4 3.1 1995 1 US-07-903-446-2 1767 1 US-07-903-466-2 1767 2 US-08-317-944-2 3.1 1767 5 PCT-US93-05794-2 44.2 3.1 30.18 1 US-07-903-466-1 143.6 3.0 4852 1 US-07-903-466-1 143.6 3.0 2830 2 US-09-010-928B-1 3 3.0 3223 1 US-07-983-913-3 4 3 3.0 3233 1 US-07-980-528-1 3 43 3.0 51259 3 US-08-781-891-209 42.8 3.0 765 4 US-09-605-785-524
ACGAGGTTGTCCTGGACAGG 465	ATTTGCCCATTGC 285	ength 1757;	Sequence 1, Appli Sequence 2, Appli Sequence 4, Appli Sequence 93, Appli Sequence 93, Appli Sequence 93, Appli Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 1, Appli Sequence 1, Appli Sequence 3, Appli Sequence 1, Appli Sequence 209, Appli Sequence 209, Appli Sequence 524, Appli

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                                                                                                                              ; LENGTH: 3262
; TYPE: DNA
; ORGANISM: HOMO Sapiens
US-09-561-989-9
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                                                                Query Match
Best Local Similarity
                                                   Matches 214;
                                                                                                                                                                                                          SOFTWARE:
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION: APPLICANT: KOLLER,
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 9, Application US/09561989 Patent No. 6468750
                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/561,989
CURRENT FILING DATE: 2000-04-27
                                                                                                                                                                                                                                                                                                         FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                      APPLICANT: KOLLER, Klaus-Peter
TITLE OF INVENTION: No. 6468750el Cell Regulation Factor TTO20
                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1246 GCGGGGCTGGAGGAGGAGCGCCTGGACGTGCCAGAAGG 1283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1160 GAAGGGAAGGAAGGACCACCAGTAAGGAGCTGGATG 1197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1040 GACTTCTTTACTTTGGATTTAGAGCACATAGCAGACGCCCTGAGAGCCATTGACTTTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1126 GAGCAATTCTCTGTGAGCGTGGACCACGTGGCCGAAATGTTGCGAACCATCGACTTCCAG
563 AGCACCTCATGTGTGAGGAGCACGAGGACGAGAAGATCAACATCTACTGCCTGAGCTGCG 622
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAGGTTTTCGGCGCCCACAAGGACTGTGAGGTGGCCCCTCTGCCCACCATTTACAAACGC 705
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                                                                                                                                                                                                                               PatentIn Ver. 2.0
                                               Conservative
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                                                                4.98;
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                                                              Score 70; DB 4;
Pred. No. 1.4e-07;
                                             Mismatches 240;
                                                                                  DB 4; Length 3262
                                           Indels
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; LOCATION: (1)..(1926)
; OTHER INFORMATION: coding strand of EBNA-1 DNA
US-09-249-585A-2
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; LENGTH: 1926
; TYPE: DNA
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/09249585A Patent No. 6417002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Horlick, Robert
TITLE OF INVENTION: METHOD FOR MAINTENANCE AND SELECTION OF EPISOMES
FILE REFERENCE: 0867/0D905
CURRENT APPLICATION NUMBER: US/09/249,585A
CURRENT FILING DATE: 1999-02-11
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Epstein Barr Virus
                               940 GGCCTCATCCGCCAGTACGGAGACCACTTGGAGGGCTCCTCAAAGCTGGTGGAGTCCGCC 999
                                                                                                                                                                                                                                                              760 GTGCAGGCAGTGATCACCCAGATGGAGGAGGTGTGCCAGACCATTGAGGACAACAGCCGC 819
                                                                       880 AAGGGCGAACTGCTTCAAGCACTGGCCCGGGAGCAGGAGGAGGAAGTTGCAGCGCGTGCGG
                                                                                                                                                 820 AGACAGAAGCAACTGTTAAACCAGAGGTTCGAGACCCCTGTGCGCGGTTTTGGAGGAGCGC 879
                                                                                                                                                                                                                              749 GTCTCATGGAGTACTGCTTGGAGGTGATTAAGGA 782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 923 AGTTGCAGCGCGTGCGGGGCCTCATCCGCCAGTACGGAGACCACTTGGAGGGCTCCTCAA 982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       629 ATGCCCTCAACAGAAGAAAAGCCCAGCTGCTGGCCCGCGTCAACAAGGAGCATGAGCACA
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                                                                                                                                                                                                                                                                                                                             Local Similarity
CGGTTTTGGAGGAGCGCAAGGGCGAACTGCTTCAAGCACTGGCCCGGGAGCAGGAGGAGA 922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTCTGCCCACCATTTACAAACGCCAGAAGAGTGAGCTGAGCGATGGCATCGCGATGCTGG 742
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                                                                                                                                                                                                                                                                                                           237;
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                                                                                                                                                                                                                                                                                                                           4.7%;
                                                                                                                                                                                                                                                                                                       0; Mismatches 284;
                                                                                                                                                                                                                                                                                                                         Score 66.6; DB 4; Length 1926; Pred. No. 7.7e-07;
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                                                                                                                                               ; MOLECULE TYPE: US-09-050-863-2
Вb
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                                                                                         Query Match
Best Local Similarity
                                                                       Matches
                                                                                                                                                                                                                                                                           TELEFAX: (415) 949-8711 INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-65
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Hiang, Betty
APPLICANT: Payan, Don
TITLE OF INVENTION: Manumalian Protein Interaction Cloning
TITLE OF INVENTION: System
NUMBER OF SEQUENCES: 5
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APPLICATION NUMBER: US/
FILING DATE: 30-MAR-199
CLASSIFICATION:
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                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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CITY: San Francisco
                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
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                                                                                         4.78;
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                                                                       Score 66.6; DB 3;
Pred. No. 8.5e-07;
0; Mismatches 284;
                                                                                                          Length 2580;
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US-09-359-081-2
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                 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1240 GGCAATGCGGGGCTGGAGGAGGAGCGTGCCAGA 1280
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                                                                                                                                                                                                                                                                                                                            ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/050,863
FILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-65638/DJB/RMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Mammalian Protein Interaction Cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Lao, Ying
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                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 949-8711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTCCAGCCGGGCGCCGCTGGGGATGAAGAGGATGACGACATGGCTTTGGATGGGGAGGAG 1239
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                                                                                                                                                                                                                                                                     CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/359,081 FILING DATE: 22-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: San Francisco
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 4 Embarcadero Center, Suite 3400
LENGTH: 2580 base pairs
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Payan, Don
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; LENGTH: 5452
; TYPE: DNA
; ORGANISM: VEBNA
US-09-130-114-1
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US-09-130-114-1/c
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    Query Match
Best Local Similarity
Matches 237; Conserv
                                                                                                                               \begin{array}{c} \text{SOFTWARE: FastSEQ for Windows Version 3.0} \\ \text{SEQ ID NO 1} \end{array}
                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/09130114 Patent No. 5976807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
'rocal Similarity
                                                                                                                                                            APPLICANT: Horlick, Robert A.
APPLICANT: Damaj, Bassam B.
APPLICANT: Damaj, Bassam B.
APPLICANT: Robbins, Alan K.
TITLE OF INVENTION: Eukaryotic Cells Stably Expressing
TITLE OF INVENTION: From Multiple Transfected Episomes
FILE REFERENCE: 0867/1D903US1
CURRENT APPLICATION NUMBER: US/09/130,114
CURRENT FILING DATE: 1998-08-06
NUMBER OF SEQ ID NOS: 36
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MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTCCAGCCGGCCCCCTGGGGATGAAGAGGATGACGACATGGCTTTGGATGGGGAGGAG 1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGGCAGGAGGGAGCAGGAGGGGGGAGGGGGGAGGA 1193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: unknown
      Conservative
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45.5%;
                  4.78;
   0;
 Score 66.6; DB 2;
Pred. No. 1.1e-06;
0; Mismatches 284;
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                               Length 5452;
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US-08-910-647-1
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                           TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION: APPLICANT: Zuckeri
                                                                                           REFERENCE/DOCKET NUMBER: 12
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,64
                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                       STREET: 4000
STREET: Emeryville
CITY: Emeryville
STATE: California
                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
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                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                             TELEPHONE:
                                                                                                                                                                           CLASSIFICATION: 514
                                                                                                                                                                                                                                             SOFTWARE:
                                                                                                                               REGISTRATION NUMBER:
                                                                                                                                                 NAME:
                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                             ZIP:
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                LENGTH:
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94608-2916
                                                                                                                    /AGENT INC...
Fujita, Sharon M.
Fujita, Sharon M.
12
nucleic acid
             9600 base pairs
                                                                                                                                                                                                                                                                                                                                                                                      4560 Horton Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zuckermann et al.
                                                                             (510) 923-2706
                                                                                                                                                                                                                                                                                                                                                                                                         Chiron Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Compositions and Methods
                                                                                                                                                                                                           US/08/910,647
                                                                                                              1218.002
                                                                                                                                                                                                                                           Version
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STRANDEDNESS: single

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                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09620925
Patent No. 6468986
GENERAL INFORMATION:
APPLICANT: Zuckermann et al.
TITLE OF INVENTION: Compositions and Methods for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 237;
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        ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/620,925
FILING DATE: 21-U1-2000
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
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ADDRESSEE: Chiron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAGGGCGAACTGCTTCAAGCACTGGCCCGGGAGCAGGAGGAAGTTGCAGCGCGTGCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATCCAGTCCATGGAGGAGCCGCAGATGGCTCTCTACCTCCAGCAGGCAAAGGAGCTGATC 1059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Emeryville
                                                                                                                                                                                                          COUNTRY: U.S.A.
                                                                                                                                                                                                                          STATE: California
                                                                                                                                                                                                                                                            STREET: 4560 Horton Street
APPLICATION NUMBER: 08/910,647
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Pred. No. 1.3e-06;
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                                                                                                                                                                                                       RESULT 9
US-07-884-811-15
                                                                                                                                                                      Sequence 15, Application US/07884811 Patent No. 5316921
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SEQUENCE CHARACTERISTICS:
LENGTH: 9600 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1000
                                                                                                    APPLICANT: Godowski, Paul J. Lokker, Nathalie A. TITLE OF INVENTION: SINGLE-CHAIN HEPATOCYTE GROWTH NUMBER OF SEQUENCES: 21
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                                                                 CORRESPONDENCE ADDRESS: ADDRESSEE: Genentech,
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Local Similarity 45.5%;
les 237; Conservative (
                                               STREET:
COUNTRY:
                STATE:
                                CITY:
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              South San Francisco
California
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                                                 460 Point San Bruno Blvd
 USA
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Pred. No. 1.3e-06;
                                                                                                                                         Lokker, Nathalie A.
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FACTOR VARIANTS
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RESULT 10
US-07-885-971-15
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Best Local Similarity
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                                                                                                 1240 GGCAATGCGGGGCTGGAGGAGGAGCGGCTGGACGTGCCAGA 1280
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                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Dreger, Ginger R.
REGISTAGEN NUMBER: 33,055
REFERENCE/DOCKET NUMBER: 75:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-3216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 1992051
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                           1000 ATCCAGTCCATGGAGGAGCCGCAGATGGCTCTCTACCTCCAGCAGGCAAAGGAGCTGATC 1059
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      940
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 880 AAGGGCGAACTGCTTCAAGCACTGGCCCGGGAGCAGGAGGAGAAGTTGCAGCGCGTGCGG 939
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 10596 bases
TYPE: NUCLEIC ACID
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                GGGCAGGAGGGCAGGAGCAGGAGGGGGGGGGAGGA 2773
                                                                                                                                   AGCATGGAGCAATTCTCTGTGAGCGTGGAGCACGTGGCCGAAATGTTGCGAACCATCGAC 1179
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ilarity 45.5%;
Conservative
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Sequence 15, Application US/07885971

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TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 15
SEQUENCE CHARACTERISTICS:
LENGTH: 10596 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No. 5328837
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                                                                                                                                                                                                        1000
1180 TTCCAGCCGGGCGCCGCTGGGGATGAAGAGGATGACGACATGGCTTTGGATGGGGAGGAG 1239
                                                                                                                                                                       2493
                                                                                                                                 1060 AACAAGGTCGGGGCAATGTCGAAGGTGGAGCTGGCAGGACGGCCGGAGCCAGGCTATGAG
                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 inch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                               820 AGACAGAAGCAACTGTTAAACCAGAGGTTCGAGACCCTGTGCGCGGTTTTGGAGGAGCGC 879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 530 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Godowski, TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                 880 AAGGGCGAACTGCTTCAAGCACTGGCCCGGGAGCAGGAGGAGAAGTTGCAGCGCGTGCGG 939
                                                                                                                                                                                                                                                                                                                                                                                                                                                     760 GTGCAGGCAGTGATCACCCAGATGGAGGAGGAGGTGTGCCAGACCATTGAGGACAACAGCCGC 819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   y Match 4.7%;
Local Similarity 45.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Dreger, Ginger R. REGISTRATION NUMBER: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER:
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                                                                                                                                                                  AGCATGGAGCAATTCTCTGTGAGCGTGGAGCACGTGGCCGAAATGTTGCGAACCATCGAC 1179
                                                                                                ATCCAGTCCATGGAGGAGCCGCAGATGGCTCTCTACCTCCAGCAGGCAAAGGAGCTGATC 1059
                                                                                                                                                                                                                                                                 GGCCTCATCCGCCAGTACGGAGACCACTTGGAGGGCTCCTCAAAGCTGGTGGAGTCCGCC 999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       237;
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches 284;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 66.6; DB 1;
Pred. No. 1.3e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 10596;
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US-08-087-783A-15
                                                                                                                                                                                                                                                              Matches 237;
                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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REFERENCE/DOCKET NUMBER: P0755779P1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/884811
FILING DATE: 18-MAY-92
PRIOR APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inch, 1.44 mb floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 2
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                                                                                             880 AAGGGCGAACTGCTTCAAGCACTGGCCCGGGAGCAGGAGGAGGAAGTTGCAGCGCGTGCGG 939
                                                                                                                                                           820 AGACAGAAGCAACTGTTAAACCAGAGGTTCGAGACCCTGTGCGCGGTTTTGGAGGAGCGC 879
                                                                                                                                                                                                                        760 GTGCAGGCAGTGATCACCCAGATGGAGGAGGTGTGCCAGACCATTGAGGACAACAGCCGC 819
                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 410/371-7168
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TELEPHONE: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                        TYPE: Nucleic Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 07 FILING DATE: 18-MAY-92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/087,783A FILING DATE: 13-Jul-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 460 Point San Bruno Blvd CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE:
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                              GGCCTCATCCGCCAGTACGGAGACCACTTGGAGGGCTCCTCAAAGCTGGTGGAGTCCGCC 999
                                                              GGGCAGGAGGAGGAGGAGGAGGAGGGGCAGGA 2773
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WENTION: HEPATOCYTE GROWTH FACTOR VARIANTS
                                                                                                                                                                                                                                                              Conservative
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                          Score 66.6; DB 1;
Pred. No. 1.3e-06;
0; Mismatches 284;
                                                                                                                                                                                                                                                            284;
                                                                                                                                                                                                                                                                                          Length 10596;
                                                                                                                                                                                                                                                          Indels
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US-08-194-088B-15
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                                                                                                                                                 US-08-194-088B-15
                                                                      Query Match 4.7%;
Best Local Similarity 45.5%;
Matches 237; Conservative
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                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 75
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-2614
APPLICATION NUMBER: 07/8 FILING DATE: 18-MAY-1992 ATTORNEY/AGENT INFORMATION: NAME: Gallegos, R. Thoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 530 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                   760 GTGCAGGCAGTGATCACCCAGATGGAGGAGGAGGTGTGCCAGACCATTGAGGACAACAGCCGC 819
                                                                                                                                                                                                                                                                          TELEPHONE: 415/225-26
TELEFAX: 415/952-9881
TELEX: 910/371-7168
                                                                                                                                                                                 LENGTH: 10596 bases
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: 09-FEI
                                                                                                                                                                                                                                                                                                                                                                            NAME: Gallegos, R. Thomas REGISTRATION NUMBER: 32,6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER:
                                                                                                                                                                       TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGCAATGCGGGGCTGGAGGAGGAGCGCCTGGACGTGCCAGA 1280
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                                                                                                                                                                     linear
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    Paul J. Lokker, Nathalie A. Mark, Melanie
SINGLE-CHAIN HEPATOCYTE GROWTH FACTOR VARIANT

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                                                                      Score 66.6; DB 1;
Pred. No. 1.3e-06;
0; Mismatches 284;
                                                                                                          Length 10596;
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US-08-194-087-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 inch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Godowski, TITLE OF INVENTION: |
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                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: 415/225-3216
                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                           TELEPHONE: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 460 Point San Brun CITY: South San Francisco STATE: California
                                                                                                                                        REGISTRATION NUMBER: 33, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                       FILING DATE:
STRANDEDNESS:
                                                                                                                                                                       NAME:
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                        LENGTH:
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                                                                          910/371-7168
                           10596 bases
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                                                                                                                                                                                                                                                                                                                                                              360 Kb floppy disk
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RESULT 14
PCT-US93-04648-15
; Sequence 15, Application PC/TUS9304648
; GENERAL INFORMATION:
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Best Local Similarity
             APPLICATION NUMBER: 07, FILING DATE: 18-MAY-92 PRIOR APPLICATION DATA: APPLICATION NUMBER: 07,
                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                           SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Genentech, Inc., Godowski, TITLE OF INVENTION: HEPATOCYTE GROWTH
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                                                                                                              APPLICATION NUMBER: POFILING DATE: 19930517
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460 Point San Bruno Blvd
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18-MAY-92
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45.5%;
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TELECOMMUNICATION INFORMATION: TELEPHONE: 415/225-3216

415/952-9881

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REFERENCE/DOCKET NUMBER:

ATTORNEY/AGENT INFORMATION:

NAME: Dreger, Ginger R. REGISTRATION NUMBER: 33,055

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US-09-249-585A-4/c
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                                                                            GENERAL INFORMATION:
APPLICANT: HOTLICK, ROBERT
TITLE OF INVENTION: METHOD FOR MAINTENANCE AND SELECTION OF EPISOMES
FILE REFERENCE: 0867/00905
CURRENT APPLICATION NUMBER: US/09/249,585A
CURRENT FILING DATE: 1999-02-11
NUMBER OF SEQ ID NOS: 18
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                                                                                                                                                                                                   Sequence 4, Application US/09249585A Patent No. 6417002
                                                SOFTWARE: PatentIn version 3.0 SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
ORGANISM: Epstein
                TYPE: DNA
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                                ENGTH: 1926
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TELEX: 910/371-7168
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TYPE: NUCLEIC ACID
STRANDEDNESS: single
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Local Similarity 45.5%;
nes 237; Conservative
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Best Local Similarity 44.9%;
                                                                                                                                                                                                                                                                 Sequence 2, Application US/09130114 Patent No. 5976807
              SEQ ID NO 2
LENGTH: 1931
                                                                APPLICANT: Horlick, Robert A.
APPLICANT: Damaj, Bassam B.
APPLICANT: Dobins, Alan K.
TITLE OF INVENTION: Eukaryotic Cells Stably Expressing Genes
TITLE OF INVENTION: From Multiple Transfected Episomes
FILE REFERENCE: 0867/1D903USI
CURRENT APPLICATION NUMBER: US/09/130,114
CURRENT FILING DATE: 1998-08-06
NUMBER OF SEC ID NOS: 36
                                                      SOFTWARE: FastSEQ for Windows Version 3.0
TYPE: DNA
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Pred. No. 3.2e-06;
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US-08-232-463-14/c
US-08-232-463-14/c
: Sequence 14, Application US/08232463
: Patent No. 5670367
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US-09-130-114-2
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                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                               APPLICANT: DORNER, r.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
TITLE OF SPOHENCES: 52
        COUNTRY: USA
ZIF: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati)
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                                                                                                                                      STREET:
   OPERATING SYSTEM:
                                                                                                                                                      ADDRESSEE:
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Local Similarity 44.9%;
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                                                                                                                                   E: Foley & Lardner
1800 Diagonal Road
PC-DOS/MS-DOS
                                                                                                                                   Road,
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Pred. No. 3.2e-06;
                                                                                                                                   Suite
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RESULT 18
US-08-728-323A-1
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Sequence 1, Application US/08728323A Patent No. 5948676
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               1041 GCAGGCAAAGGAGCTGATCAACAAGGTCGGGGCAATGTCGAAGGTGGAGCTGGCAGGACG 1100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               981 AAAGCTGGTGGAGTCCGCCATCCAGTCCATGGAGGAGCCGCAGATGGCTCTCTACCTCCA 1040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: BENT, Stephen A. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                               GGGATGCTGAGGATCTGCGCAGAGACCACCGCGCCACCAAGCTCGGCTTCCCGCC 1395
                                                                                                                                                                                                                                                                                                                                 AATGTTGCGAACCATCGACTTCCAGCCGGGCGCCCCCTGGGGATGAAGAGGATGACGACAT 1220
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                                                                                                    RRRRRRRRRRRRRRRRRRRRRRRRRRATCGCAAGCTCCCTCGACCTGCAGCC
                                                                                                                                                                  AGGCTCAGGCCTGCACTGACCCGACTCTGATCCAGAGCGCACACCCGAAGCGGGAGCCAA 1340
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ER: 30472/114 IMMU
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GENERAL INFORMATION:

APPLICANT:

Chang, Yuan Bohenzky, Roy A. Russo, James J.

APPLICANT:

TITLE OF INVENTION:

Immediate Early Protein From Kaposi's Sarcoma-Associated Herpesvirus, DNA

APPLICANT: Edelman, Isidore S. APPLICANT: Moore, Patrick S

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INFORMATION FOR SEQ ID NO: 1:
2396 AGCAGGAGCAGGAGTTAGAGGAGCAGGAGCAGGAGTTAGAGGAGCAGGAGCAGGAGTTAG 2455
                                         1121 GCATGGAGCAATTCTCTGTGAGCGTGGAGCACGTGGCCGAAATGTTGCGAACCATCGACT 1180
                                                                                                                             1061 ACAAGGTCGGGGCAATGTCGAAGGTGGAGCTGGCAGGACGGCCGGAGCCAGGCTATGAGA 1120
                                                                                                                                                                              2276 AGGAGCAGCAGGAGCAGGAGCAGGAGTTAGAGGAGCAGGAGCAGGAGTTAGAGGATC
                                                                                                                                                                                                                                                                 2216 ATGAGCAGCAGCAGGATGAGCAGCAGCAGGATGAACAGGAGCAGCAGGAGGAGC 2275
                                                                                                                                                                                                                                                                                                                                                       2156 AGCAGGATGAGCAGCAGCAGCAGGATGAGCAGCAGCAGGATGAGCAGCAGCAGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                             2096 AGCAGGAGCAGGATGAGCAGGAGCAGGATGAGCAGGAGCAGCAGGATGAGCAGC 2155
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ATTORNEY/AGENT INFORMATION:
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NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 212-391-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: sing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: White, John P. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
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APPLICANT: Ballestas, Mary E.
APPLICANT: Ballestas, Mary E.
APPLICANT: Ballestas, Mary E.
APPLICANT: Ballestas, Mary E.
APPLICANT: Kaye, Kenneth M.
TITLE OF INVENTION: REPLAY OF THE TRANS ON A UNIT OF RHADINO TITLE OF INVENTION: VIRUS DNA TO MEDIATE EFFICIENT EPISOME PERSISTENCE FILLE REPERENCE: 16412-10001R
CURRENT APPLICATION NUMBER: US/09/298,568
CURRENT FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 60/109,422
EARLIER FILING DATE: 1998-11-19
NUMBER OF SEC 10 NOC. 2
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1241 GCAATGCGGGGCTGGAGGAGGAGGGGCTGGACGTGCCAGAAGGCTCAGGCCTGCA 1295
                                                    2456 AGGAGCAGGAGCTAGAGGAGCAGGAGCAGGAGTTAGAGGAGCAGGAGCAGGAGT 2515
                                                                                                           1181 TCCAGCCGGGCGCCGCTGGGGATGAAGAGGATGACGACATGGCTTTGGATGGGGAGGAGG 1240
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les 257;
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Similarity 43.2%;
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Pred. No. 0.0008;
"Amatches 338; Indels
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Best Local Similarity
Matches 257; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (212) 278-0400
TELEPAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 32207 base pairs
TYPE: nucleic acid
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APPLICANT: Chang, Yuan
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19781 ATGAGCAGCAGCAGCAGGATGAGCAGCAGCAGCAGGATGAACAGGAGCAGCAGCAGGAGGAGC 19722
                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 52
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: POLYPEPTIDES TITLE OF INVENTION: HERPESVIRUS,
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                                                                                                                                                                                                                                                                                                   761 TGCAGGCAGTGATCACCCAGATGGAGGAGGTGTGCCAGACCATTGAGGACAACAGCCGCA 820
                                      941 GCCTCATCCGCCAGTACGGAGACCACTTGGAGGGCTCCTCAAAGCTGGTGGAGTCCGCCA 1000
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STATE: New Yorl
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ZIP: 10036
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TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
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                                                                                   AGGGCGAACTGCTTCAAGCACTGGCCCGGGAGCAGGAGGAGGAAGTTGCAGCGCGTGCGGG 940
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Russo, James J.
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43.2%; Pred. No. 0.0015;
vative 0; Mismatches 338; Indels
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19481 TAGAGGAGCAGGAGGTGGAAGAGCAAGAGCAGGAGGTGGAAGAGCAAGAGCAGGA 19427
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                                                           1241 GCAATGCGGGGCTGGAGGAGGAGCGGCTGGACGTGCCAGAAGGCTCAGGCCTGCA 1295
                                                                                                                                                                                                                                                                                                                                GCATGGAGCAATTCTCTGTGAGCGTGGAGCACGTGGCCGAAATGTTGCGAACCATCGACT 1180
                                                                                                                                                                                                 TCCAGCCGGGCGCCCTGGGGATGAAGAGGATGACGACATGGCTTTGGATGGGGAGGAGG 1240
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Search completed: December Job time: 194 secs 3, 2002, 09:13:33

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Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model
Run on:

December 3, 2002, 09:05:22; Search time 64 Seconds
(vithout alignments)
Beforec:

US-09-908-988B-1
Perfect score:

1431
Sequence:

IDENTITY_NUC
Gapop 10.0, Gapext 1.0
Searched:

341543 seqs, 192557720 residues

Total number of hits satisfying chosen parameters:

683086
Minimum DB seq length: 0
Maximum Match 100%
Maximum Match 100%
Maximum Match 100%
Maximum Match 150
Maximum Match 15
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Sequence 20, Appl	Sequence 53, Appl	Sequence 54, Appl	Sequence 3972, Ap	Sequence 5584, Ap	Sequence 812, App	Sequence 115, App	Sequence 115, App	Sequence 41, Appl	Sequence 56, Appl	Sequence 4, Appli	Sequence 25, Appl	Sequence 482, App	Sequence 493, App	Sequence 34, Appl	Sequence 3, Appli	Sequence 21, Appl	Sequence 5, Appli	Sequence 1, Appli	Description

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Sequence 173, App Sequence 616, App	· —	<u>. </u>	ا سر		Sequence 326, App	Sequence 326, App	Sequence 326, App	Sequence 225, App	Sequence 225, App	Sequence 225, App	Sequence 225, App	Sequence 177, App	Sequence 524, App	Sequence 524, App	Sequence 524, App	Sequence 225, App	Sequence 2, Appli		Sequence 167, App	Sequence 6282, Ap				

ALIGNMENTS

	QY 181 GCTCCAGAGCGCGGGGATGAACTTCACGGTGGGTTTCAAGCCGCTGCTAGGGGATGCG 240	QY 121 TGACCGAGGAAGGGTGCACAGGCAGGGGAGAAGGCCAACGACGAGGAGAGGCAG 180	Qy 61 GACAGGACTCTTCCAAGAGGGAGCAATAGCCGGGATCCCAAGAATCCAGTCAGCCTAAAC 120	Oy 1 AAGGAGTGTAGACAGAGTGTCTGGAAATAGACAGGGGTGAGAGGAGCTGTTAGGGGAAGG 60	Query Match 100.0%; Score 1431; DB 10; Length 1431; Best Local Similarity 100.0%; Pred. No. 0; Matches 1431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	PRICHART NO. USZUVZULZ/039041 GENERAL INFORMATION: APPLICANT: OLSON, ERIC APPLICANT: SPENCER, JEFFREY A. APPLICANT: SPENCER, JEFFREY A. APPLICANT: SPENCER, JEFFREY A. TITLE OF INVENTION: IN STRIATED MUSCLE CELLS FILE OF INVENTION: IN STRIATED MUSCLE CELLS FILE REFERENCE: MYOG:028US CURRENT APPLICATION NUMBER: US/09/908,988B CURRENT FILING DATE: 2000-07-18 PRIOR APPLICATION NUMBER: 60/219,020 PRIOR FILING DATE: 2000-07-18 ORGANISM: DATE: DONOS: 6 SOFTWARE: Patentin Ver. 2.1 LENGTH: 1431 TYPE: DNA ORGANISM: Mus musculus FEATURE: NAME/KEY: CDS LOCATION: (199)(1296)	US-09-908-988B-1; Sequence 1, Application US/09908988B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: SPENCER, JEFFREY A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STABILIZING MICROTUBULES
TITLE OF INVENTION: IN STRIATED MUSCLE CELLS
FILE REFERENCE: MYOG:028US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: CDS
LOCATION: (299
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TYPE: DNA
ORGANISM: Mus musculus
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Best Local :
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                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ23
CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                    LENGTH: 1781
TYPE: DNA
ORGANISM: Homo s
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                                                                  TGTGCCAACGACGTCTTCCAGGCCTCTAATCCTCTGTGGCAATCCCGGGGCTCCACAACG
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   GTGTCTTCAGGAGGACGTTTCCGATGCCCATCTTGTAGGCACGAGGTTGTCCTGGACAGG
                                 TGTGCCAATGACATCTTCCAGGCTGCAAATCCCTACTGGACCAGCCGGGCCAGCTCAGTG
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                                                                                                                                                          ACAGATGAGGAAGAGGAAGTTCATTGAAGAAGAAGATCAGGAAGAGGAAGAGTCCACA 1153
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RESULT 4
US-09-908-988B-3
; Sequence 3, Application US/09908988B
; Patent No. US20020127690A1
; GENERAL INFORMATION:
   APPLICANT: OLSON, ERIC
   APPLICANT: SPENCER, JEFFREY A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STABILIZING MICROTUBULES
; TITLE OF INVENTION: IN STRIATED MUSCLE CELLS
; FILE REFERENCE: MYOG:028US
; CURRENT APPLICATION NUMBER: US/09/908,988B
; CURRENT ETLING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/219,020
; PRIOR FILING DATE: 2000-07-18
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; NAME/KEY: CDS
; LOCATION: (80)..(1714)
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Best Local Similarity 63.8%;
Matches 702; Conservative
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SOFTWARE: PatentIn Ver. 2.1
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ORGANISM: Mus musculus
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                                                                       TTGGAGGGCTCCTCAAAGCTGGTGGAGTCCGCCATCCAGTCCATGGAGGAGCCGCAGATG 1026
                                                                                                                    CGGGAGCAGGAGGAGAAGTTGCAGCGCGTGCGGGGCCTCATCCCGCCAGTACGGAGACCAC
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                                                                                                    CGAACACAGGAGGAGAAACTGGAACATGTCCGAACTCTTATCAGGAAGTATTCCGATCAC
                                                                                                                                                            TTTGATCACCTATACGGCATCCTGGAGGAGGGAAGACTGAAATGACCCAAGCCATCACT
                                                                                                                                                                                                                                                                           GACTGTGAGGTGGCCCCTCTGCCCACCATTTACAAACGCCAGAAGAGTGAGCTGAGCGAT 726
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Pred. No. 4e-99;
0; Mismatches 392; Indels 6;
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; Sequence 34, Application US/09764864

; Patent No. US20020132753A1
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LENGTH: 1762
TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/764,864 CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and
FILE REFERENCE: PTZ23
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----GAAAAGAAATCCGACCAGCCCATGTGCGAGGAACATGAAGAGGGAGCGCATCAACAT
                                                                                           GCACGCCAAGGCTGAACAGCACCTCATGTGTGAGGAGGACGACGACGAGAAGATCAACAT
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                                                                                                                                             GAGGAACCTGCTGGTGGAAAATATCATTGACATCTACAAGCAGGAGTCCACCAGGCCA--
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64.7%;
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Sequence 493
Patent No. US20020132753A1
GENERAL INFORMATION:
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                                                                                                                                                          SEQ ID NO 493
LENGTH: 587
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                       Query Match
                                                                                                                                                                                                                                                   Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 1792
                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/764,864 CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                          APPLICANT: Rosen et al. TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PTZ23
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                                 187 GAGCGCCGCGGATGAACTTCACGGTGGGTTTCAAGCCGCTGCTAGGGGATGCGCACAAC 246
 124 GACAGCGAGGAGATRAGCGCATCTCTGAATTACAAATCTTTTTCCAAAGAGCAGCAGACC 183
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hes 333;
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                                                                       Conservative
                                                                                        16.0%;
                                                                 Score 229.2; DB iv,
Pred. No. 3.8e-46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 482, Application US/09764864 Patent No. US20020132753A1
                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Prior application data removed - consult PALM or NUMBER OF SEQ ID NOS: 1792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/764,864 CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: SITE
LOCATION: (362)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (400)
OTHER INFORMATION: n equals a,t,g, or c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 446
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                                                                                                                                                                                                                226 CTGCTAGGGGATGCGCACAACATGGACAACTTGGAGAAGCAGCTCATTTGCCCCCATCTGC 285
                    406
                                                                                                                                              286 CTGGAGATGTTCTCCAAGCCCGTGGTGATCTTGCCCTGCCAACACACAACCTGTGCCGCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATGGACAACTIGGAGAAGCAGCTCATTIGCCCCATCTGCCTGGAGATGTTCTCCAAGCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCCTCTAACCCGTATTTGCCCCACAAGAGGAGGTACCACCATGGCATCAGGGGGCCGATTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGATGCCCATCTTGTAGGCACGAGGTTGTCCTGGACAGGCATGGTGTCTATGGCCTGCAG 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCCTCTAATCCTCTGTGGCAATCCCGGGGCTCCACAACGGTGTCTTCAGGAGGACGTTTC
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                                                                                      TGTGCCAACGACGTCTTCCAGGCCTCTAATCCTCTGTGGCAATCCCGGGGCTCCACAACG
                                                                                                                                                                                            CTGATCCAGGATGGGAATCCCATGGAGAACTTGGAGAAGCAGCTGATCTGCCCTATCTGC 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TACTGCCTGAGCTGCGAGGTGCCCACCTGCTCTCTCTGCAAGGTTTTCGG 656
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                                                     CTGGAGATGTTTACCAAGCCAGTGGTCATCTTGCCGTGCCAGCACAACCTGTGCCGGAAG
GTGTCTTCAGGAGGACGTTTCCGATGCCCATCTTGTAGGCACGAGGTTGTCCTGGACAGG
                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                   11.3%;
72.5%;
                                                                                                                                                                                                                                                                    0,
                                                                                                                                                                                                                                                                                     Score 162; DB 10;
Pred. No. 4.7e-30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and Antibodies
                                                                                                                                                                                                                                                                        82;
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US-09-880-192-25
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Best Local Similarity
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SOFTWARE: PERL Program
SEQ ID NO 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 25, Application US/09880192 Patent No. US20020077470A1
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CURRENT FILING DATE: 2001-06-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Azimzai, Yalda
TITLE OF INVENTION: POLYNUCLEOTIDES ASSOCIATED WITH CARDIAC MUSCLE FUNCTION
FILE REFERENCE: PB-0009-1 CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Walker, michael G. APPLICANT: Volkmuth, Wayne APPLICANT: Klingler, Tod M. APPLICANT: Azimzai, Yalda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1039
                                        1268 TGGACGTGCCAGAAGG 1283
                                                                                                                                                                                                                                                                                                                                                                    1028
                                                                                                                                                                                                                                               242
422 AGTAAGGAGCTGGATG 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       848 TCGAGACCCTGTGCGCGGTTTTGGAGGAGCGCAAGGGCGAACTGCTTCAAGCACTGGCCC 907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          378 CACGGAGTGTACGGGCTGGCAANAAGAACTGCTGGGTGGAAAACATCATCCACATCTACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  438 AACAAG 443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 AGGAGCAGGAGAAAAAGCTTAGCTTCATCGAGGCCCTCATCCAGCAGTACCAGGAGCAGC 121
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                                                                            AGGATGACGACATGGCTTTGGATGGGGAGGAGGAGGAGGAGGAGGAGGAGGGGC 1267
                                                                                                                                                                                                                                         GCCAGCTGGGGAAGACAGAGCAGGGCTTTGAGAACATGGACTTCTTTACTTTGGATTTAG
                                                                                                                                                                                                                                                                             AGCTGGCAGGACGGCCGGAGCCAGGCTATGAGAGCATGGAGCAATTCTCTGTGAGCGTGG 1147
                                                                                                                                                                                                                                                                                                                   CCACCTTCCTTGACTGCCAAGCAACTCATCAAAAGCATTGTGGAAGCTTCCAAGGGCT 241
                                                                                                                                                                                                                                                                                                                                                         CTCTCTACCTCCAGCAGGCAAAGGAGCTGATCAACAAGGTCGGGGCAATGTCGAAGGTGG 1087
                                                                                                                                                        AGCACATAGCAGACGCCCTGAGAGCCATTGACTTTGGGACAGATGAGGAAGAAGAAT
                                                                                                                                                                                                AGCACGTGGCCGAAATGTTGCGAACCATCGACTTCCAGCCGGGCGCCCCCTGGGGATGAAG 1207
                                                                                                                                                                                                                                                                                                                                                                                                    TGGACAAGTCCACAAAGCTGGTGGAAACTGCCATCCAGTCCCTGGACGAGCCTGGGGGAA 181
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57.88;
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Pred. No. 4.9e-25;
D; Mismatches 184
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RESULT 9

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                                                                                                                                                                                                       Sequence 56, Application US/09764864 Patent No. US20020132753A1
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                     CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or
NUMBER OF SEQ ID NOS: 1792
                                                                                                         APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ23
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  SOFTWARE:
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PRIOR APPLICATION NUMBER: CN01106406.4
PRIOR FILING DATE: 2001-01-02
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn version 3.1
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CURRENT FILING DATE: 2001-10-04
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APPLICANT:
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TYPE: DNA
ORGANISM: Nephila clavipes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1183 CAGCCGGGCGCCGCTGGGGATGAAGAGGATGACGACATGGCTTTGGATGGGGAGGAGGAGGGC 1242
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                                                                                                                                                                                                                                                                                                                                                                                      1243 AATGCGGGGCTGGAGGAGGAGCGGCTGGACGTGCCAGA 1280
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PatentIn Ver. 2.0
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Li, Wei
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; ORGANISM: Homo sapiens
US-09-764-864-56
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LENGTH: 140
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Patent No. US20020077470A1
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LENGTH: 3441
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APPLICANT: Klingler, Tod M.
APPLICANT: Azimzai, Yalda
TITLE OF INVENTION: POLYNUCLEOTIDES ASSOCIATED
FILE REFERENCE: PB-0009-1 CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/880,192
CURRENT FILING DATE: 2001-06-12
NUMBER OF SEQ ID NOS: 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PERL Program
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Incyte ID No. US20020077470A1 4151935CB1
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NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                    1148 CCACTGACAAGGTGTTTGGCACCCACAAAGACCATGAAGTTTCAACGCTTGACACAGCTA 1207
                                                                                                                                                                                                                                                                                                                                        1088 AAGAGCTGAAAAAGTCCCAGATTGACACATACTGTTACACCTGCAAATGTCCCAATTTCTG 1147
                                                                                                                                                          1208 TAAGTGCTGTAAAGGTTCAATTAGCAGAATTTCTAGAAAATTTACAAGAAAAGTCCTTGA 1267
                                                                                                                                                                                                                                                                                                                                                                                  578 AGGAGCACGAGAAGATCAACATCTACTGCCTGAGCTGCGAGGTGCCCACCTGCT 637
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Local Similarity 51.3%;
hes 118; Conservative
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GCAGACAGAAGCAACTGTTAAACCAGAGGTTCGAGACCCTGTGCGCGGGTTTTGGAGGAGC 877
                                                                                                                                                                                                                                                                         CTCTCTGCAAGGTTTTCGGCGCCCACAAGGACTGTGAGGTGGCCCCTCTGCCCACCATTT 697
                                                                      GGATTGAAGCCTTTGTTAGTGAGATAGAATCCTTTTTTAATACCATTGAGGAAAACTGTA 1327
                                                                                                              GTGTGCAGGCAGTGATCACCCAGATGGAGGAGGTGTGCCAGACCATTGAGGACAACAGCC 817
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Pred. No. 0.0033;
0; Mismatches 112; Indels 0;
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Pred. No. 0.0055;
0; Mismatches 256;
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LENGTH: 7065
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APPLICANT: Brannon, Mark
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANI
FILE REFERENCE: 210121.420C9
FULL REFERENCE: 210121.420C9
CURRENT FAPLICATION NUMBER: US/09/91,496
CURRENT FILING DATE: 2001-11-20
NUMBER OF SEQ ID NOS: 137
SOFTWARE: FastSEQ for Windows Version 4.0
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                                       1203 TGAAGAGGATGACGACATGGCTTTGGATGGGGAGGAGGCCAATGCGGGGGCTGGAGGAGGA 1262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          846 GTTCGAGACCCTGTGCGCGGTTTTGGAGGAGCGCAAGGGCGAACTGCTTCAAGCACTGGC 905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   906 CCGGGAGCAGGAGGAGAGTTGCAGCGCGCGTGCGGGGCCTCATCCGCCAGTACGGAGACCA
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                                                                                   CGCCGAGGAGCTG----CAGCAGCGCCTAGACACCGCCACGCAGCAGCGCGCGCGAGCTGGA
                                                                                                                             CGTGGAGCACGTGGCCGAAATGTTGCGAACCATCGACTTCCAGCCGGGCGCGCCGCTGGGGA 1202
                                                                                                                                                                         GGTGGAGCTGGCAGGACGGCCGGAGCCAGGCTATGAGAGCATGGAGCAATTCTCTGTGAG 1142
                                                                                                                                                                                                                                                                                                         GATGGCTCTCTACCTCCAGCAGGCAAAGGAGCTGATCAACAAGGTCGGGGCAATGTCGAA 1082
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Skeiky, Yasir A.W.
Bhatia, Ajay
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Pred. No. 0.026;
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SEQ ID NO 115
LENGTH: 7065
TYPE: DNA
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APPLICANT:
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CURRENT FILING DATE: 2001-06-04
NUMBER OF SEQ ID NOS: 122
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APPLICANT: Brannon, Mark
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
FILE REFERENCE: 210121.420C8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Leishmania major and chagasi
2547 GGCACAGGTGGCACGGCTGGCCGCGACCGACGAGGCCCGCCAGCAGCTGGCCGGAA 2606
                                                                                                               1143
                                                                                                                                                                                                                                                    1023 GATGGCTCTCTACCTCCAGCAGGCAAAGGAGCTGATCAACAAGGTCGGGGCAATGTCGAA 1082
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                    TGAAGAGGATGACGACATGGCTTTGGATGGGGGAGGAGGAGGAGGAGGAGGA 1262
                                                                                                        CGTGGAGCACGTGGCCGAAATGTTGCGAACCATCGACTTCCAGCCGGGCGCCCCCTGGGGA 1202
                                                                      CGCCGAGGAGCTG---CAGCAGCGCCTAGACACCGCCACGCAGCAGCGCGCCGAGCTGGA
                                                                                                                                                                                 GGTGGAGCTGGCAGGACGCCGGAGCCAGGCTATGAGAGCATGGAGCAATTCTCTGTGAG 1142
                                                                                                                                                                                                                  GTTCGAGACCCTGTGCGCGGTTTTGGAGGAGCGCAAGGGCGAACTGCTTCAAGCACTGGC 905
                                                                                                                                             GGCACAGGTGGCACGGCTGGCCGCGGACCGCGACGAGCGCGCCAGCAGCTGGCCGCGAA
                                                                                                                                                                                                                                                                                         GGAGGCACAGTTGGCACGGCTGGCCGCGGACCGACGAGGCGCCGCCAGCAGCTGGCCGC
                                                                                                                                                                                                                                                                                                                         CTTGGAGGGCTCCTCAAAGCTGGTGGAGTCCGCCATCCAGTC---CATGGAGGAGCCGCA 1022
                                                                                                                                                                                                                                                                                                                                                              CCGGGAGCAGGAGAAGTTGCAGCGCGTGCGGGGCCTCATCCGCCAGTACGGAGACCA 965
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Skeiky, Yasir A.W.
Bhatia, Ajay
Coler, Rhea
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PRIOR FILING DATE: 2001-01-16

PRIOR APPLICATION NUMBER: US 60/300,111

PRIOR FILING DATE: 2001-06-22

NUMBER OF SEQ ID NOS: 5379

SEQ ID NO 812

LENGTH: 768

TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-938-842A-812
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
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654 CGGTGGTGG
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                                 AGCGGCTGG 1270
                                                                                                     ATGAAGAGGATGACGACATGGCTTTGGATGGGGAGGAGGCAATGCGGGGCTGGAGGAGG
                                                                                                                                        TGGAGGAGGAGGTTCTGGCGAAGGAGGAGCTCATGGTGGTTGCTTACGGAGCAGGAGGTGG
                                                                                                                                                                                                                                            AGGTGGAGCTGGCAGGACGGCCGGAGCCAGGCTATGAGAGCATGGAGCAATTCTCTGTGA 1141
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                                                                 AGCTGGAGAGGGATACGGTGGTGGTGCTGGAGCTGGTGGACATGGTGGAGGAGGAGGAGG
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Zhu, Tong
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45.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches 201;
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US-09-864-761-3972
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APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Kamigaki, Laura Y. (Ito)
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLECTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
FILE REFERENCE: PL-0012-1 CON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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APPLICANT:
                                                                                                                                                                                            APPLICANT: Hanzel, David K.

APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
                                         PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
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PRIOR FILING DATE: 1998-05-05
NUMBER OF SEQ ID NOS: 6332
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CURRENT FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: 09/298,329
PRIOR FILING DATE: 1999-04-21
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LOCATION: 62-88
OTHER INFORMATION: a,
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OTHER INFORMATION: Incyte ID No. US20020013958A1 700457287H1
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TYPE: DNA
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                       APPLICATION NUMBER: PCT/US01/00666
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Similarity 54.8%;
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Hanzel, David K.
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2001-01-30
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Pred. No. 0.023;
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JOTHER INFORMATION: EXPRESSED US-09-864-761-3972
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OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 10
OTHER INFORMATION: EXPRESSED IN BYA74, SIGNAL = 11
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 11
OTHER INFORMATION: EXPRESSED IN LING, SIGNAL = 11
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 07
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 17
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 9.4
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 9.4
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                                             1272 CGTGCCAGAAGGCTCAGG 1289
                                                                                                                                          1212 TGACGACATGGCTTTGGATGGGGAGGAGGGCAATGCGGGGGCTGGAGGAGGAGCGGCTGGA 1271
                                                                                                                                                                                                                                1152 CGTGGCCGAAATGTTGCGAACCATCGACTTCCAGCCGGGCGCCGCTGGGGATGAAGAGGA 1211
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                                                                                                                                                                                                                                                                                     312 CTCCCTCCTGCAGAGAACAGGACTAGGCCAGCACTGGCCCCAGAAGTGGAGCAGTAAGAAGG 371
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FILING DATE: 2000-09-21
APPLICATION NUMBER: US 09/608,408
FILING DATE: 2000-06-30
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00662
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FILING DATE: 2001-01-30
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GGAAGGAGGAGGAAGAGG
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132; Conserv
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IN HEART, SIGNAL = 9.4
IN HBL100, SIGNAL = 11
IN FETAL LIVER, SIGNAL =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 45.2; DB 10;
pred. No. 0.082;
0; Mismatches 123;
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US-09-71-161A-54 ; Sequence 54, Application US/09771161A ; Patent No. US20020110811A1

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RESULT 18
US-09-771-161A-53
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; Patent No. US20020110811A1
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; LOCATION: (1)..(1464);
; OTHER INFORMATION: "n"
US-09-771-161A-54
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CURRENT APPLICATION NUMBER: US/09/771,161A
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 09/724,676
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 136776
PRIOR APPLICATION NUMBER: 136776
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 135619
PRIOR APPLICATION NUMBER: 135619
PRIOR APPLICATION NUMBER: 135619
PRIOR FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 273
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Best Local Similarity 44.78;
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TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
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ORGANISM: Homo sapiens
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                                                                                                                            CGGCTGCTGCGAGAAGAGCTCGCTGCGGCCTCCTCCGCTTCAGCACCCCGCCTGGCC
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Pred. No. 0.16;
0; Mismatches 317;
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TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
FILE REFERENCE: 802620-2005.1
CURRENT APPLICATION NUMBER: US/09/771,161A
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 09/724,676
PRIOR FILING DATE: 2000-11-28
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 135619
PRIOR FILING DATE: 2000-04-12
NUMBER OF SE0 ID NOS: 273
SOFTWARE: Patentin version 3.0
SEQ ID NO 53
LENGTH: 2518
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Best Local Similarity 44.7%;
Matches 263; Conservative
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GGGCCCTTTCCCGCCACGCACTACAGCACCCTGTGCAAGCCCGCGCCGC
                                       GGCTCCTCAAAGCTGGTGGAGTCCGCCATCCAGTCCATGGAGGAGCCGC 1021
                                                                                 CGGCTGCTGCGAGAAGAGCTCGCTGCGGCCTCCTCCGCTGCCTTCAGCACCCGCCTGGCC
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Pred. No. 0.19;
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RESULT 19 US-09-771-208-20/c

GENERAL INFORMATION:

APPLICANT: MEDRANO, JUAN

APPLICANT:

BRADFORD, ERI HORVAT, SIMON Sequence 20, Application US/09771208 Patent No. US20020155564A1

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                                                                                                                             NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.0
SEQ ID NO 20
                                                             CURRENT APPLICATION NUMBER: US/09/771, 208
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: US 08/999,477
PRIOR FILING DATE: 1997-12-29
                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: (13280)..(132700)
OTHER INFORMATION: n is unidentified a,
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                                                                                            1160 AAATGTTGCGAACCATCGACTTCCAGCCGGGCGCCGCTGGGGATGAAGAGGATGACGACA 1219
                                                                                                                                                              1100 GCCCGGAGCCAGGCTATGAGAGCATGGAGCAATTCTCTGTGAGCGTGGAGCACGTGGCCG 1159
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OTHER INFORMATION: n is a, c, g, or t
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LOCATION: (183872)...(183891)
OTHER INFORMATION: n is unidentified
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LOCATION: (346860)...(346823)
OTHER INFORMATION: n is unidentified
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LOCATION: (170625)..(170645)
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OTHER INFORMATION: n is unidentified
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OTHER INFORMATION: n is unidentified
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OTHER INFORMATION: n is unidentified
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LOCATION: (494715)..(494814)
OTHER INFORMATION: n is unidentified
NAME/KEY: misc_feature
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LOCATION: (546998)..(547017)
OTHER INFORMATION: n is unidentified
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LOCATION: (602466)..(602485)
OTHER INFORMATION: n is unidentified
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OTHER INFORMATION: n is unidentified
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                              TGGCTTTGGATGGGGAGGAGGCCAATGCGGGGCTGGAGGAGGA 1262
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OTHER INFORMATION: Clone ID: 27-LIB3058-020-Q1-K1-G3
US-09-960-352-6282
Search completed: December
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SEQ ID NO 6282
LENGTH: 319
TYPE: DNA
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEAR AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
FILE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Warren, Wesley C. APPLICANT: Tao, Nengbing
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                                                                                                                                                                                                                                                                                                                   1146 GGAGCACGTGGCCGAAATGTTGCGAACCATCGACTTCCAGCCGGGCGCCGCTGGGGATGA 1205
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                                                                                                                     GCTGGACGTGCCAGAAGGCTCAGGCCTGCACTGACCCG 1303
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Job time : 1350 secs

Gaps

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Copyright (c) 1993 - 2002 Compugen Ltd. Unto 1995 A.
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OM nucleic - nucleic search, using sw model December 3, 2002, 10:09:37; Search time 2857 Seconds

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14576.869 Million cell updates/sec

Scoring table: OLIGO_NUC US-09-908-988B-1 1431 1 aaggagtgtagacagagtgt.....ataaaggactcaagtgtccc 1431 Gapop 60.0 , Gapext 60.0

Title: Perfect score:

Sequence:

Run

Searched: 2054640 segs, 14551402878 residues

Word size : 3

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : gb_pat:* gb_ph:* gb_pr:* gb_htg: jb_om:* *: un_dg gb_sy:* gb_sts:* *:or_dg

em_or:*
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Pred. No. is the number of results predicted by chance to have

em_htgo_hum:*
em_htgo_mus:*
em_htgo_other:*

em_htg_vrt:* em_htg_mam: * em_htg_rod:* em_htg_pln:* em_htg_mus:*

em_htg_hum:*
em_htg_inv:*
em_htg_other:*

em_vi:*

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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16173 29952 40834 72305 74317 87463		1597 196461 1776 1776 1810 1925 2098 2209 2098 2203 2634 121721 121721 121721 13372 3372 13372 153005 15723	Length 1431 1448 209211 199296 49743 164772 1329 118847
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F262 C012 A124 A124 CB13 CC12F	280 023 023 250 076 076 050 050	AX418852 ALG27314 AB047601 BC007750 HSA243488 AK091728 HSA291712 AK091310 AC021240 AC021240 AC021240 AC0212718 AC0212718 AC0213718 AC0213718 AC0213718 AC0213718 AC0213718 AC0213841 AC0213841 AC0213841 AC0213841 AC0213841	AX41848 AF294790 AC084883 - AC114519 - AC114519 - AC195184 AC095184 AC095184 AC03291714 HSA2391714 HSA2391714 AC06663 AC025662
			1-3471) 1006 denty 1006 denty 1006 denty 1007 denty 534-711
262977 262977 012715 242593 513465 451017 731579	AC128011 Rattus no AC12387 Mus muscu AC102387 Mus muscu AC093136 Pan trogl AC025065 Homo sapi AC107613 Homo sapi AC122289 Mus muscu AJ336987 Homo sapi Z79968 H.sapiens CAE010904 Methanosa AC014410 Drosophil	4,1852 Sequence 6627314 Mouse 047601 Macaca 007750 Homo sa 24348 Homo sa 24348 Homo sa 291712 Homo sa 291712 Homo sa 291712 Homo sa 291712 Homo sa 291714 Homo sa 291716 Homo sa 021240 Homo sa 011976 Homo sa 011976 Homo sa 015718 Ho	Criptio 118848 S 294790 84883 M 114619 M 114619 M 114619 M 114619 M 113413 H 113413 H 113413 H

ALIGNMENTS

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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	i; Muridae;	Sciurognath	Rodentia;	lia; Eutheria;	Mamma	
Euteleostomi;	'ertebrata;	Craniata; V	Chordata;	<pre>Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;</pre>	Eukar	
				Mus musculus	Mus n	ORGANISM
				house mouse.	house	SOURCE
						KEYWORDS
			3712	AX418848.1 GI:21523712	AX418	VERSION
				848	AX418848	ACCESSION
		318.	ent W00206	Sequence 1 from Patent W00206318	Seque	DEFINITION
PAT 18-JUN-2003	linear	op DNA	1431 bp	848	AX418848	LOCUS

RESULT 1 AX418848 LOCUS

REFERENCE AUTHORS Olson, E.N. and Spencer, J.A. Methods and compositions for stabilizing microtubules and intermediate filaments in striated muscle cells

TITLE

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                                                             AACATCTACTGCCTGAGCTGCGAGGTGCCCACCTGCTCTCTGCAAGGTTTTCGGCGCC
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RESULT 2 AF294790 LOCUS VERSION KEYWORDS REFERENCE SOURCE DEFINITION ACCESSION ORGANISM Mus

Mus musculus.

musculus

Chordata; Rodentia;

Craniata; Vertebrata; Sciurognathi; Muridae;

Muridae;

Euteleostomi;

Murinae;

Richardson, J.A. and

differentiation

AF294790 Mus musculus RING-finger AF294790 GI:9945009 1448 bp 1448 bp mRNA protein MURF mRNA, linear complete ROD 08-SEP-2000

Eukaryota; Metazoa; (Mammalia; Eutheria; 1 1 (bases 1 to 1448) Olson, E.N. Spencer, J.A., Eliazer, S., Ilaria, R.L. Jr.,

TITLE

Regulation of microtubule dynamics and myogenic

150 (4), 771-784 (2000)

muscle RING-finger

protein

JOURNAL MEDLINE MURF, a striated J. Cell Biol. 150 20411220

PUBMED REFERENCE AUTHORS TITLE 10953002

JOURNAL

2 (bases 1 to 1448)
Spencer, J.A. and Olson, E
Direct Submission
Submitted (09-AUG-2000)
Blvd., Dalfas, TX 75390-1 to 1448)
.A. and Olson, E. TX 75390-9148, USA ż Biology, UTSW,

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	480 480	21 CGTTTCCGATGCCCATCTTGTAGGCACGAGGTTGTCCTGGACAGGCATGGTGTCTATGGC	Qy 4:
	420 420	61 TTCCAGGCCTCTAATCCTCTGTGGCAATCCCGGGGCTCCACAACGGTGTCTTCAGGAGGA	Qy 36
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                                            AC084883

209211 bp DNA linear Musculus chromosome 5 clone RP23-154K6 strain DRAFT SEQUENCE, 21 unordered pieces.
             HTG; HTGS_PHASE1; HTGS_DRAFT
                        AC084883.10 GI:17976433
                                  AC084883
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SOURCE ORGANISM REFERENCE

REFERENCE AUTHORS TITLE AUTHORS JOURNAL 2 (bases 1 to 209211)
Han,J., Montgomery,K.T., Grills,G., Chiu,D., Decker,J., Fusina Goltz,J., Haider,A., Hall,L., Ioshikhes,I.P., Lee,E., Long,J., Perera,A., Shim,C., Thomas,E. and Kucherlapati,R.

Direct Submission High Mus musculus Han,J., Montgomery,K.T., Grills,G., Chiu,D., Decker,J., Goltz,J., Haider,A., Hall,L., Ioshikhes,I.P., Lee,E., Louis, A., Shim,C., Thomas,E. and Kucherlapati,R. Unpublished Mammalia; Eukaryota; Metazoa; mmalia; Eutheria; Rodentia; Sciurognathi; Muridae; (bases 1 to 209211) Throughput Mouse Sequencing Chordata; Craniata; Vertebrata; Euteleostomi; Lee, E., Long, J., Murinae; Mus Fusina, M., Fusina, M.,

TITLE JOURNAL

Submitted (29-NOV-2000) Department of Molecular Genetics, Albert Einstein College of Medicine Genome Center, 1300 Morris Park Ave.,

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FEATURES
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Chemistry: Dye-terminator Big Dye; 100%
*Consensus quality: 204023 at least Q20
*Consensus quality: 203326 at least Q30
*Consensus quality: 203766 at least Q40
*Setimated insert size: 308811 - sum-of-contigs
Quality coverage: agarose-FP - N/A
Quality coverage: 10.2 x in Q20 bases; sum-of-contigs estimation
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On Dec 21, 2001 this sequence version replaced gi:15148085.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site: http://www.hpcgg.org/Sequence/mouse.html
Contact: hpgc@mendel.mgh.harvard.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center Code:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: This is a 'working draft' sequence. It currently consists of 21 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Harvard Partners Genome Center
                    /strain="C57BL6/J"
       /db_xref="taxon:10090"
                                        /organism="Mus musculus"
                                                                             location,
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11: contig of 1350
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41: contig
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241 CACAACATGGACAACTTGGAGAAGCAGCTCATTTGCCCCATCTGCCTGGAGATGTTCTCC
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Db 190949
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ORIGIN
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GCTCCAGAGCGCCGCGGGATGAACTTCACGGTGGGTTTCAAGCCGCTGCTAGGGGATGCG
                 GCTCCAGAGCGCCGCGGGATGAACTTCACGGTGGGTTTCAAGCCGCTGCTAGGGGATGCG
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/note="assembly_name:Contig28"
199082. .201315
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30176. .76428
                                                                                                                                                                                                                                                                                                                                                                                          /note="assembly_name:Contig20"
                                                                                                                                                                                                                                                                                                                                                                                                                 206944.
                                                                                                                                                                                                                                                                                                                                                                                                                             note="assembly_name:Contig21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="assembly_name:Contig22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="assembly_name:Contig23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="assembly_name:Contig24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="assembly_name:Contig26"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="assembly_name:Contig27"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 171576.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="assembly_name:Contig33"
161529. .171555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  133816.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="assembly_name:Contig35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="assembly_name:Contig36"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note="assembly_name:Contig25"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="assembly_name:Contig29"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="assembly_name:Contig30"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note="assembly_name:Contig31"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="assembly_name:Contig32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="assembly_name:Contig34"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="assembly_name:Contig37"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note-"assembly_name:Contig38"
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5. .147516
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                                                       12 3 (bases 1 to 199296)

13 (bases 1 to 199296)

14 Saliren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landzaree, R., Landzers, T., Lehozzky, J., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Mathews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Riback, M., Rilay, R., Rise, C., Rogov, P., Rogerti, M., Roye, A., Santos, R., Rilay, R., Rise, C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (10-MAR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus, clone RP24-86I23
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                             Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S.,
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Seaman, S., Severy, P., Spencer, B.,
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Stange-Thomann, N.,
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                                                                                                                  FEATURES
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                                                                            source
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Submitted (06-JUN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jun 6, 2002 this sequence version replaced gi:19311148. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               by the finished sequence as soon as it is available and the accession number will be preserved.

728: contig of 728 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                               59590 79430: contig of 19841 bp in length 79431 79530: gap of 100 bp 79531 99545: contig of 20015 bp in length 99546 99645: gap of 100 bp 99646 123290: contig of 30645 bp in length 123291 123390: gap of 100 hp 123391 151687.
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Center clone name: 86_I_23

Center clone name: 86_I_23

Center clone name: 86_I_23

Center clone name: 86_I_23

Sequencing vector: Plasmid; n/a; 100% of reads chemistry: Dye-terminator Big Dye; 100% of reads chemistry: 19147 bases at least Q40

Consensus quality: 197247 bases at least Q20

Consensus quality: 197247 bases at least Q20
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                                                                                                                                                                                                                                       Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34035 44466: contig of 100 bp 10 length 44467 44566: gap of 100 bp 100 b
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Insert size: 197896; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                         151688 151787: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6052 6151: gap of 100 bp 6152 10082; contig of 3931 bp in length 10083 10182: gap of 100 bp 10183 18316; contig of 8134 bp in length 18317 18416; gap of 100 bp 100
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/organism="Mus musculus"
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6051: contig of 2148 bp in length
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/db_xref="taxon:10090"

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RESULT 5
AC114541/c
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SOURCE
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                                                                                        REFERENCE
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                   REFERENCE
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                                                      AUTHORS
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                                                                                                                                                                                                                                                                                                                                  TGCAGCGCGTGCGGGGCCTCATCCGCCAGTACGGAGACCACTTGGAGGGCTCCTCAAAGC 985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 236;
                                                                                                                                                                         49743 bp DNA Mus musculus clone RP23-89G3, LOW-PASS AC114541 AC114541. GI:19311061 HTG: HTGS PHACEA
                                                Birren,B., Linton,L., Nusbaum,C. and Lander,E. Mus musculus, clone RP23-89G3
Birren, B., Linton, L., Nusbaum, C., Lander, E.,
                                                                                                                                          Mus musculus
                                Unpublished
                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                (bases 1 to 49743)
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6152. 10082
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99646. .123290
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10183. .18316
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100.0%; Pred. No. 3.7e-119;
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Ali, A., Allen, N.,
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Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., MacGonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Maneus, L., Mihova, T., Meneus, L., Mihova, T., Meneus, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Raymond, C., Retta, R., Rieback, M., Riley, R., Schauer, S., Schupback, R., Seaman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigillo, J., Vassiliev, H., Viel, R., Vo, A., Willson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Direct, Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (10-MAR-2002) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Boukhgalter, B., Brown, A., Camarate, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              * NOTE: This record contains 62 individual
* sequencing reads that have not been assembled into
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
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714 813: gap of 100 bp
814 1529: contig of 716 bp in length
1530 1629: gap of 100 bp
1630 2320: contig of 691 bp in length
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3883 3982: gap of 100 bp
3983 4708: contig of 726 bp in length
4709 4808: gap of 100 bp
4809 5518: contig of 710 bp in length
100 bp in 1072 bp in 1075 bp in 1
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2420: gap of 100 bp
3085: contig of 665 bp in length
3185: gap of 100 bp
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1924: gap of 10
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18352: cont
   373: gap
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33679: contig of 705 bp
779: gap of 100 bp
34485: contig of 706 bp
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19168: contig of 716 bp
168: gap of 100 bp
19983: contig of 715 bp
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28061: contig
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85 unordered piece
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Mammalia; Eutheria; Rodentia; Sciurognathi;
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Direct Submission
Direct Submission
Submitted (11-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
of Molecular And Human Genetics, Baylor College of Medicine, One
of Molecular and Human Genetics, Baylor College of Medicine, One
of Molecular and Human Genetics, Baylor College of Medicine, One
of Molecular and Human Genome Sequencing Center, Department
of Molecular and Molecul
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Worley,K.C.
Direct Submission
Submitted (16-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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                                                                                                                                                                                                                                                                  Contact: hgsc-help@bcm.tmc.edu

Center project Information
Center project name: CDAW
Center clone name: CH230-9D7

Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 79000 bases at least 040
Consensus quality: 85421 bases at least 030
Consensus quality: 90756 bases at least 020
                                                          arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                     as soon as it is available and the accession number be preserved.
                                                                                                                              (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 85 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                             NOTE: Estimated insert size may differ from sequence length
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Center code: BCM
Web site: http://
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                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1329)
Centner,T., Yano,J., Kimura,E., McElhinny,A.S., Pelin,K., Witt,C.C., Bang,M.L., Trombitas,K., Granzier,H., Gregorio,C.C., Sorimachi,H. and Labeit,S.
Identification of muscle specific ring finger proteins as potential regulators of the titin kinase domain J. Mol. Biol. 306 (4), 717-726 (2001)
                                       Submitted (12-FEB-2001) Centner T., EMBL-Heidelberg, Meyerhofstrasse 1, Revised by author 22-FEB-2001
                                                                                                                                                                                                                                                         Homo sapiens mRNA for RNF30 gene for ring AJ291714
                                                                                Centner,T
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              University School of Medicine, MO 63108, USA
                                                   Direct Submission
Submitted (09-NOV-1999) Genome
                                                                                                      Unpublished (2001)
3 (bases 1 to 118847)
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AC013413
                                                                                  Waterston, R.H.
                                                                                                                                         Swearengen, S. and Kozlowicz, A. The sequence of Homo sapiens B
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Sulston, J.E. and Waterston, R.
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LAREQEEKLQRVRGLIRQYGDHLEASSKLVESAIQSMEEPQMALYLQQAKELINKVGA
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TOMBEVCOTIEDNSRROKOLLTORFESLCAVLEERKGELLQALAREQEEKLQRVRGLI
RQYGDHLEASSKLVESAIQSMEEPOMALYLQQAKELINKVGAMSKVELAGRPEPGYES
MEQFIVRVEHYAEMLATIDFOPGASGEEEEVAPDGEEGSAGPEEERPDGP"
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49. .1203
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/protein_id="CAC32841.
/db_xref="GI:13160388"
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KAEQHLMCEEHEEEKINIYCLSCEVPTCSLCKVFGAHKDCEVAPLPTIYKRQKKQDLT
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/protein_id="CAC32842.1"
/db_xref="GI:13160389"
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5 (bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The RPCI-11 human BAC library was made from the blood of one male donor, as described by Oscegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and Coworkers at http://www.chori.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. McPherson additional information about the map position of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                RP11-538J11 contains a transposon in the growth of the clone which has been omitted from the finished sequence. Data from AC025662 was used to finish this clone, AC013413.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    The clone sequenced to the left is RP11-195B17, 2000 bp overlap. Actual start of this clone is at base position 80914 of RP11-195B17; actual end is at base position 118847 of RP11-538J1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (21-FEB-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63 On Jan 16, 2002 this sequence version replaced gi:16418272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Waterston, R.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOURCE INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence, see http://genome.wustl.edu/gsc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center project name: H_NH0538J11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: sapiens@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://genome.wustl.edu/gsc
                              /note="
                                                                          /note="match to EST AI978781
133. .154
                                                                                                                                                                                                                                                     /db_xref="taxon:9606"
/chromosome="2"
      /note="similar to Mus
                                                                                                                                                                                       /clone_lib="RPCI-11"
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                                                                                                                                           note="match to EST
                                                                                                                                                                                                         /clone="RP11-538J11"
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                                                match to EST BG256909 (NID:g12766725)"
                                                                                                                                    BE789511 (NID:g10210709)"
    musculus EST BB659249
                                                                                          (NID:g5803811) wr59f04.x1"
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(NID:g11619948)"
5859. .5931
                       /rpt_family="Alu" 6428. .6450
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5187. .5329
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2971. .3156
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(NID:915575755)"
1991. .2327
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/note="similar to Mus musculus
(NID:910493072)"
                                                                                                                               /note="similar to
(NID:g12108987)"
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3359. .3667
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404. .626
                                                                                                                                                                                                     /note="match
                                                                                                                                                                                                                                                                                                                                                            /note="similar to Mus musculus EST BF532585 (NID:g11619948)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="similar to Mus musculus (NID:g15575755)"
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(NID:916493072)"
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(NID:915575755)"
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                                                                                     note="match to EST
                                                                                                                                                                                                                                                                                                                  note="match to EST BM152742 (NID:g17177267)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="match to EST BE242145"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (NID: g16493072)
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                                                                     .6450
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to EST BE789511 (NID:g10210709)"
                                                                                                                                                                                                     to EST BE242145 (NID:g9093794)
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                                                                                        AI244159
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                                                                                     (NID:g3839556) qj80e03.x1"
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RESULT 9
AX060632
                      RESULT 10
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TITLE
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                                                                                                    777
                                                                                                                                      685 CTGCCCACCATTTACAAACGCCAGAAGAGTGAGCT 719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                              Local
                                                                                                  CTGCCCACCATTTACAAACGCCAGAAGAGTGAGCT 811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 54 from Patent W00078954.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AX060632.1 GI:12406053
    AC025662
                                                                                                                                                                                                                                                                                                                                                                   Lal.P., Yue,H., Tang,Y.T., Baughn,M.R., Azimzai,Y. and Tran,B. Human transcriptional regulator proteins Patent: WO 0078954-A 54 28-DEC-2000; Incyte Genomics, Inc. (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human
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                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
378 c 439 g 28
                                                                                                                                                                                                                                                                                                                                    1. .1500
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6556. .6741
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                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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Pred. No.
      123280 bp.
                                                                                                                                                                              Mismatches
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      DNA
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      linear
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      HTG 13-APR-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (12-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Apr 13, 2000 this sequence version replaced gi:7230272.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Young, G., Zainoun, J., Zimmer, A. and Zody, M. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Birren,B., Linton,L., Nusbaum,C. and Lander,E. Homo sapiens, clone RP11-352I22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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AC025662.2 GI:7547186
                                                                                                                                                                                                                                                                    NOTE: This record contains 146 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that
  2490: contig of 710 bp in length
2491 2590: gap of 100 bp
2591 378: contig of 788 bp in length
3379 3478: gap of 100 bp
4239: contig of 788 bp in length
4240 4339: gap of 100 bp
4340 513: contig of 761 bp in length
4340 513: contig of 761 bp in length
                                                                                                                                                                                                                                    be preserved.
                                                                                                                                                                                                                                                      the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center clone name: 352_I_22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center code: WIBR
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1619: cc
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                                                                                                                                                                                                                  748:
of 100 bp contig of 774 bp in length
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Homo sapiens clone RP11-352I22, LOW-PASS SEQUENCE SAMPLING.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 123280)
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Anderson S., Baldwin, J., Barna, N., Bastien, V., Beda, F.,
Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G.,
Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S.,
Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S.,
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Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Tasfmer, A., and Zodv, M., Wyman, D., Ye, W.J.,
Young, G., Zajnoun, J., Zinmer, A., and Zodv, M. 2 (bases 1 to 123280)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,

Center: Whitehead Institute/ MIT Center for Genome Research

of 100 bp contig of 771 bp in length contig of 748 bp in length

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547 25324: contig of 778 bp 1
325 25424: gap of 100 bp
125 26211: contig of 778 bp in
12 26311: gap of 100 bp in
12 26311: gap of 100 bp in
12 27074: contig of 786 bp in
15 2774: gap of 100 bp
16 28925: contig of 786 bp in
17 28025: contig of 785 bp in
18 28925: contig of 797 bp in
19 28925: contig of 797 bp in 1
29822: gap of 100 bp
29822: gap of 100 bp
30598: contig of 776 bp in 1
30698: gap of 100 bp
31472: contig of 774 bp in 1e
31572: gap of 100 bp
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33 45522: contig of 790 bp ir

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40255: contig of 767
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42968: gap of 100 k
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                                                                      together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one MI3 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em. EMBL; Sw:, SMISSPROT: TT:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (09-JUL-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk on Jul 10, 2002 this sequence version replaced gi:18152585. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         intermediate filaments in striated muscle cells Patent: WO 0206318-A 5 24-JAN-2002; BOARD OF REGENTS THE UNIVERSITY OF TEXAS SYSTEM (US)
  http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-354H24 is from the RPCI-23 Mouse PAC Library
                                                         database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brown, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
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/db_xref="G1:21533717"
/translation="MDYKSSLIPDGNAMENLEKQLICPICLEMFTKPVVILPCQHNLC
/translation="MDYKSSLIPDGNAMENLEKQLICPICLEMFTKPVVILPCQHNLC
/KTANDIFQAANPYWTNRGGSVSMSGGRFRCPSCRHEVIMDRHGVYGLQRNLLVENII
DIYKQECSSRPLQKGSHPMCKEHEDEKINIYCLTCEVPTCSLCKVFGAHQACEVAPLQ
SIFQGQKTELSNCISMLVAGNDRVQTIISQLEDSCRVTKENSHQVKEELSQKFDTLYA
SIFQGQKTELSNCISMLVAGNDRVQTIISQLEDSCRVTKENSHQVKEELSQKFDTLYA
SIFQGQKTELLQRITQEGEEKLGFIEALILQYREQLEKSTKLVETAIQSLDEPGGATFL
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/db_xref="taxon:10090"
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Best Local Similarity
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R. Site1: DraIII (CACTGTGTG)

R. Site2: DraIII (CACCATGTG)

Description: 1st strand cDNA was primed with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTTTTT]; double-stranded cDNA was synthesized using specific 5' and 3' primers and amplified by PCR. The PCR product was digested with SfiI and size selection was performed to exclude fragments <1.5kb.The SfiII-digested PCR product was cloned into distinct DraIII sites of pME18s-FL3. XhoI sites just outside the DraIII sites can be used to isolate the CDNA insert. Libraries were constructed by Sugano et al. (University of Tokyo, Institute of Medical Science). Custom primer used for sequencing (5' end primer [CGACCTGCAGCTCTAAAAGCTGCG];

3' end primer [CGACCTGCAGCTCCAGCACCA]).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (23-AUG-2000) Katsuyuki Hashimoto, National Institute of Infectious Diseases, Division of Genetic Resources; 23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan (E-mail:khashi@nih.go.jp, URL:http://www.nih.go.jp/yoken/genebank/, Tel:81-3-5285-1111(ex.2120), Fax:81-3-5285-1181)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fis (full insert sequence).
Macaca fascicularis adult male brain parietal lobe cDNA to mRNA, clone_lib:macaque brain cDNA library QnpA clone:QnpA-10466.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
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Hashimoto,K., Osada,N., Hida,M., Kusuda,J. and Sugano,S
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Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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Contact: humquery@sanger.ac.uk
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For further details see http://www.chori.org/bacpac/home.htm
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Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LIML at: http://image.llnl.gov Series: IRAL Plate: 17 Row: d Column: 4 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.
                                                                                                                                                                                                     Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Shevchenko,Y., Wetherby.K.D., Beckstrome-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.,
Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (11-MAY-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens, clone MGC:12836 IMAGE:4110783, mRNA, BC007750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaithersburg, Maryland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
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/clone_lib="macaque brain cDNA library QnpA"
/dev_stage="adult"
567. .1244
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/db_xref="taxon:9541"
/clone="QnpA-10466"
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/protein_id="BAB12125.1"
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AJ243488
                                                                                                                                                                                                                                                                                                                                                                                 Submitted (29-JUN-1999) Gautel M.S., Physikalische Biochemie, Max-Planck-Institut fuer molekulare Physiologie, Otto-Hahn-Strasse 11, Dortmund, 44227, GERMANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Lobases 1 to 1810)
Kelly,R., Neubauer,G. and Gautel,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AJ243488.1 GI:14588845 alternative splicing; signal transduction; titin zinc-finger
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27; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A novel RING finger protein associated with titin kinase
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SDQPMCEEHEEERINIYCLKCEVPTCSLCKVFGAHKDCOVAPLTHVFQRGKSELSDGI
AILVGSNDRYVGGVISOLEDTCKTIEECCRKOKQELCEKFDYLYGILEERKNEMTOVIT
RTQEEKLEHVRALIKKYSDHLENVSKLVESGIQFMDEPEMAVFLQNAKTLLKKISEAS
KAFQMEKIEHGYZEMMNHFTYNLLNREEKIIRELDFYREDEDEEEEEGGEGEKEGEGEVG
GEAVEVEEVQTEFFGEDENPEKASELSQVELQAAPGALFVSSPEPPPALFPAADA
PVTOIGFERAPPLGGQAAAPASGSGADSEPARHIFSFSWLNSLNE"

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/db_xref="taxon:9606"
/clone="MGC:12836 IMAGE:4110783"
/tissue_type="Muscle, rhabdomyosa
/clone_lib="NIH_MGC_17"
/lab_host="DH10B-R"
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nlcrkcasdifqasnpylptrggttmasggrfrcpscrhevvldrhgvyglqrnllvg
nlidiykqestrpekksdqpmceeheeeriniyclncevptcslckvfgahkdcqvap
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/protein_id="AAH07750.1"
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/translation="MDNLEKQLICPICLEMFTKPVVILPCQHNLCRKCASDIFQASNP
LTHVFQRQKSELSDGIAILVGSNDRVQGVISQLEDTCKTIEECCRKQKQELCEKFDYL
                                                                                /product="titin zinc-finger anchoring protein"
/protein_id="CAC43019.1"
/db_xref="GI:14588846"
                                                                                                                                                                                        /function="putative role in signal transduction"
/note="50kDa isoform"
                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xxef="taxon:9606"
/cell_type="cardiomyocyte"
/tissue_type="cardiac muscle"
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                                                                                                                                              /evidence=experimental
                                                                                                                                                                  /codon_start=1
                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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                                                508 ATCATTGACATCTACAAGCAGGAGTCC 534
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ATCATTGACATCTACAAGCAGGAGTCC 382
                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission

Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7

Kazusa Kamatari, Kisarazu, Chiba 292-0812, Japan

(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; CDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sugiyama, T., Irie, R., Ótsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, K., Kikuchi, H., Kanda, K., Wagatsuma, M., Murakawa, K., Kanehori, K., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AK091728 1925 bp mRNA linear Homo sapiens cDNA FLJ34409 fis, clone HEART2001931, similar to Mus musculus RING-finger protein MURF mR
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Isogai, T. and Yamamoto, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nishi,T., Ota,T., Nakagawa,S., Senoh,A., Mizuguchi,H., Inagaki,H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AK091728.1 GI:21750167
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                                                                                                                                                                                                                        579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human cDNA sequencing project
                                                                                                Conservative
                                                                                                                                                                                                           /clone="HEART2001931"
/tissue_type="heart"
/clone_lib="HEART2"
/note="cloning vector: pmE18SFL3"
/note="441 c 498 g 407 t
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FLQNAKTLLKKISEASKAFQMEKITEHGYENMNHFTVNLNREEKITREIDFYREDDLEE
ELEGGEGEKEEEGEVGGEAVEVEEVENVQTEFPGEDENPEKASELSQVELQAAPGALE
ELEGGEGEEREEGEVGEAVEVEEVENVQTEFPGEDENPEKASELSQVELQAAFGALSVEL
ELEGEFPPALPPAADAPVTQIGFEAPPLQGQAAAPASGSGADSEPARHIFSFSWLNSL
                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                 organism="Homo sapiens"
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Witt, C.C., Bang, M.L.,

Trombitas, K., Granzier, H., Gregorio, C.C.,

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RESULT 18
HSA291712
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AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                ATCATTGACATCTACAAGCAGGAGTCC 562
                                                                                                                                                                                                                                                                                                                                                                                          1 Similarity
27; Conserv
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2202)
Centner, T., Yano, J., Kimura, E., McElhinny, A.S., Pelin, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (29-JUN-1999) Gautel M.S., Physikalische Biochemie, Max-Planck-Institut fuer molekulare Physiologie, Otto-Hahn-Strasse 11, Dortmund, 44227, GERWANY
                                                                                                                                                                     Homo sapiens mRNA for RNF29 gene for ring finger AJ291712
                                                                                       Homo sapiens
                                                                                                          human.
                                                                                                                                                  AJ291712.1
                                                                                                                                                                                                            HSA291712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alternative splicing; signal transduction; titin zinc-finger anchoring protein; tizian.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kelly, R., Neubauer, G. and Gautel, M.
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                                                                                                                           finger protein 29; RNF29 gene
                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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RKATTNPCTTPGSEGLGQTGPPGSEDSWVRKAEVAAAAASERAAVSGKETSAPAATSQ
IGFEAPPLQGQAAPASGSGADSEPAAHIFSFSWLNSLNE"
4 497 c 534 g 435 t
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EEEGGEGEKEEEGEVGGEAVEVEEVENVQTEFPGEDENPEKASELSQVELQAAPGALP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MSASLNYKSFSKEQQTMDNLEKQLICPICLEMFTKPVVILPCQH NLCRKCASDIFQASNBYLPTRGGTTMASGGRERCPSCRHEVVLDRHGVYGLQRRLLVG NILDTYKQESTRPEKKSDQPMCEHEBERINITCLNCEVPTCSLCKVFGAHKDQVAB LTHVFGRQKSELSDGLAILVGSNDRVGGVISQLEDTCKTIEECCRKQKQELCEKFDYL YGILEERKNEMTQVITRTQEEKLEHVRALIKKYSDHLENVSKLVESGIQFMDEPEMAY TGILEERKNEMTQVITRTQEEKLEHVRALIKKYSDHLENVSKLVESGIQFMDEPEMAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /evidence-experimental
/product="titin zinc-finger anchoring protein"
/protein_id="CAC43020.1"
/db_xref="GI:14588848"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:9606"
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                                                                                                                                                                                                            linear
                                                                                                                                                                                      protein 29.
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                                                                                                                                                                                                                                                                                                                                                Local
                                                             AK091310 2634 bp mRNA linear PRI 15-JUL. Homo sapiens cDNA FLJ33991 fis, clone DFNES2007332, moderately similar to Mus musculus RING-finger protein MURF mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (12-FEB-2001) Centner T., EMBL-Heidelberg, Meyerhofstrasse 1, Revised by author 22-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identification of muscle specific ring finger proteins as potential regulators of the titin kinase domain J. Mol. Biol. 306 (4), 717-726 (2001)
                                               AK091310
                                                                                                                                                                                                                                                                                                                          Similarity
27; Conser
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                       AK091310.1 GI:21749650
                                                                                                                  AK091310
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capping; fis (full insert sequence).
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GEAVEVEEVENVQTEFPGEDENPEKASELSQVELQAAPGALPVSSPEPPPALPPAADA
PVTQIGFEAPPLQGQAAAPASGSGADSEPARHIFSFSWLNSLNE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="mdnlekqlicpiclemftkpvvilpcqhnlcrkcasdifqasnptytptregtmasgerfcpsgrhevkyldrhgvgdgrnllpenijdjkgessrpekk
Stdptregttmasgerfcpsgrhevvldrhgvgdgrnllpengrgeslsdgi
Stdptregtriptregtryfgahktogvaplthvpcpgkselsdgi
AILVGSNDRVQGVISQLEDTCKTIEECCRKQKGELCEKFDYLYGILEERKNEMTQVIT
AILVGSNDRVQGVISQLEDTCKTIEECCRKQKGELCEKFDYLYGILEERKNEMTQVIT
RTQEEKLEHVRALIKKYSDHLENVSKLVESGIQFMDEPEMAVFLQNAKTLLKKISEAS
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AILVGSNDRVQGVISQLEDTCKTIEECCRKQKQELCEKFDYLYGILEERKNEMTQVIT
RTQEEKLEHVRALIKKYSDHLENVSKLVESGIQFMDEPEMAVFLQNAKTLLKKISEAS
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GEAVEVEEVENVQTEFPGEDENPEKASELSQVELQAAPGALPVSSPEPPPALPPAADA
PVTQGEVVPTGSEQTTESETPVPAAAETADPLFYPSWYKGQTRKATTNPPCTPGSEGL
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/db_xref="taxon:9606"
133. .135
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SGSGADSEPARHIFSFSWLNSLNE"
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181. .1779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="mDNLEKQLICPICLEMFTKPVVILPCQHNLCRKCASDIFQASNP
YLPTRGGTTMASGGRFRCPSCRHEVVLDRHGVYGLQRNLLVENIIDIYKQESTRPEKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="ring finger py
/protein_id="CAC32839.1
/db_xref="GI:13160385"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note-"short isoform"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="RNF29"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="ring finger protein
/protein_id="CAC32840.1"
/db_xref="GI:13160386"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="alternative"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="RNF29"
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181. .1779
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DEFINITION
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Best Local S
Matches 27
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                                                                                                      AUTHORS
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                                                                                                                                                           Mammalia, Luc...

1 (bases 1 to 121721)

Birren,B., Nusbaum,C. and Lander,E.

Birren,B., Clone RP11-366K18
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                          Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S. Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens chromosome AC090195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nagahari,K., Masuho,Y., Nagaı,K. an NEDO human cDNA sequencing project
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Isogai,T. and Yamamoto,J.
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  Dodge, S.,
                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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ilarity 100.0%;
Conservative
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dermal fibroblasts"
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/db_xref="taxon:9606"
/clone="DFNES2007332"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cell_type="normal dermal fibroblasts (Neonatal Skin)
(NHDF2564)"
  Faro, S., Ferreira, P., FitzHugh, W., Gage, D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="DFNES2"
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Pred. No.
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We 8, clone RP11-366K18, complete sequence.
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Galagan, J.,
                                                                                                      Anderson, S.,
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RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chang, J., Chang, V., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Farreira, P., FitzGerald, M., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Garadra, S., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Liu, G., MacCean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Stauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Travis, N., Trajillo, J., Voung, G., Zainoun, J., Zembek, L., Zimmer, A., and Zody, M., Direct Submission
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Barra, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B.,
Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A.,
Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S.,
Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J.,
Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B.,
Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A.,
Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K.,
Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C.,
McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V.,
Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H.,
O'Connort, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K.,
Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P.,
Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P.,
Smith, C. Snencer R. Stange-Thomann N. Stalanger, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Phunkhang, P., KIELLE, R., Schupback, K., Jerres, R., Schupback, K., Jerres, R., Schupback, K., Stojanovic, N., Talamas, J., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Smith, C., Spencer, B., Topham, K., Travers, M., Vassiliev, H., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Tesfaye, S., Theodore, J., Topham, K., Wyman, D., Young, G., Zainoun, J., Topham, M., Wu, X., Wyman, D., Young, G., Zainoun, J.,
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                                                                                                      Submitted (29-JUN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jun 29, 2002 this sequence version replaced gi:21592056. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission Submitted (26-JUN-2002) Whitehead Institute/MIT Center for Genome
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Submitted (17-FEB-2001) Whitehead Institute/MIT Center for Genome
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(bases 1 to 121721)
Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center clone name: 366_K_18
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Search completed: December 3, 2002, 12:09:29 Job time : 5217 secs
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-DB-Published_Applications_NA -QFMT-fastap -SUFFIX-rnpb -MINMATCH-0.1
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-FGAPEXT-7 -YGAPOP-10 -YGAPEXT-0.5 -DELOP-6 -DELEXT-7
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-MODEL-frame+_p2n.model -DEV-xlh
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Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Listing first 45 summaries
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Sequence 3, Appli
Sequence 34, Appl
  Sequence 5,
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RESULT 1 US-09-908-988B-1

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                                                                                                                                                                                                                                     SEQ ID NO 3
                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2000-07-18
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: OLSON, ERIC
APPLICANT: SPENCER, JEFFREY A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STABILIZING MICROTUBULES
TITLE OF INVENTION: IN STRIATED MUSCLE CELLS
FILE REFERENCE: MYOG:028US
                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/219,020 PRIOR FILING DATE: 2000-07-18
                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/908,988B CURRENT FILING DATE: 2000-07-18
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LOCATION: (199)..(1296)
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APPLICANT: SPENCER, JEFFREY A.
TITLE OF INVENTION: METHODS AND C
TITLE OF INVENTION: IN STRIATED
FILE REFERENCE: MYOG:028US
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                                                                                                                                                                                SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 34
                                                                                                                                                                                                                                                                                                                       Sequence 34, Application US/09764864 Patent No. US20020132753A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                         APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PTZ23
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Prior application data removed
NUMBER OF SEQ ID NOS: 1792
SOPTWARE DE DATE: 1792
                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/764,864 CURRENT FILING DATE: 2001-01-17
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TYPE: DNA
ORGANISM: Homo sapiens
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APPLICANT: OLSON, E
APPLICANT: SPENCER
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CURRENT APPLICATION NUMBER: US/09/908,988B
CURRENT FILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: 60/219,020
PRIOR FILING DATE: 2000-07-18
NUMBER OF SEQ ID NOS: 6
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TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STABILIZING MICROTUBULES
TITLE OF INVENTION: IN STRIATED MUSCLE CELLS
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LOCATION: (299)..(1327)
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ORGANISM: Mus musculus
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                                                            CTG-----CAGAAAGGCAGCCACCCGATGTGCAAGGAACACGAAGACGAGAAGATCAAC
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LENGTH: 1781
TYPE: DNA
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APPLICANT: Rosen et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Nucleic Acids, Proteins, FILE REFERENCE: PTZ3 CURRENT APPLICATION NUMBER: US/09/764,864 CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE:
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GAGGACTCGTGCAGAGTGACCAAGGAGAATAGCCACCAGGTGAAGGAGGAGCTGAGTCAG
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        Sequence 493, Application US/09764864
Patent No. US20020132753A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE:
                                                                                                                                                 1139 GAGGAAGAGTCCACAGAAGGAAGGAAGAA 1168
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                                                                                                                                                                                                                                                                                                                                                                             LysValGlyAlaMetSerLysValGluLeuAlaGlyArgProGluProGlyTyrGluSer 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTCATCCAGCAGTACCAGGAGCAGCTGGACAAGTCCACAAAGCTGGGAGAACTGCCATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GlnAlaValIleThrGlnMetGluGluValCysGlnThrIleGluAspAsnSerArgArg
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                                                                                                                                                                                                              ------GGGACAGATGAGGAAGAAGAATTCATTGAAGAAGAAGATCAGGAA 1138
 PTZ23
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US-09-764-864-482; Sequence 482; Application US/09764864; Patent No. US20020132753A1
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; ORGANISM: HOMO
US-09-764-864-493
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                                                                            SOFTWARE: Patentin Ver.
SEQ ID NO 482
LENGTH: 446
                                                                                                                                                                                                                                            GENERAL INFORMATION:
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LENGTH: 587
                                                                                                                                                                                        APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ23
                                                                                                                            Prior application data removed - consult PALM or NUMBER OF SEQ ID NOS: 1792
                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 1792
SOFTWARE: PatentIn Ver. 2.0
NAME/KEY:
LOCATION:
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CURRENT FILING DATE: 2001-01-17
                                            TYPE: DNA
ORGANISM: Homo
                                FEATURE:
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                                                                                                                                                                                                                                                                                                                                          CCCACCTGCTCTCTGCAAGGTGTTTGGT
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US-09-880-192-25; Sequence 25, Application US/09880192; Patent No. US20020077470A1
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DB:
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Best Local Similarity:
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                                        Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                      ; NAME/KEY: misc_feature ; OTHER INFORMATION: Incyte ID No. US20020077470A1 975169CT1 US-09-880-192-25
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US-09-908-988B-2 (1-366) x US-09-880-192-25 (1-1039)
                                                                                           Score:
                                                                                                          Pred. No.
                                                                                                                         Alignment Scores:
                                                                                                                                                                                                                                SOFTWARE: PERL Program
SEQ ID NO 25
LENGTH: 1039
TYPE: DNA
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                            APPLICANT: Walker, Michael G.
APPLICANT: Volkmuth, Wayne
APPLICANT: Klingler, Tod M.
APPLICANT: Azimzai, Yalda
TITLE OF INVENTION: POLYNUCLEOTIDES ASSOCIATED WITH CARDIAC MUSCLE FUNCTION
FILE REFERENCE: PB-0009-1 CIP
                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/880,192
CURRENT FILING DATE: 2001-06-12
NUMBER OF SEQ ID NOS: 62
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LOCATION: (400)
OTHER INFORMATION:
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                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                                                       FEATURE:
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CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR FILING DATE: 2000-03-08
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NUMBER OF SEQ ID NOS: 1890
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (293)
; OTHER INFORMATION: n equals a,t,g, or US-09-925-301-101
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APPLICANT: ROSen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins
FILE REFERENCE: PA106
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
PRIOR FILING DATE: 2000-03-08
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PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
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                                                                                         CysGlnThrIleGluAspAsnSerArgArgGlnLysGlnLeuLeuAsnGlnArgPheGlu 218
                                                                                                                                                                                                                                                                           GluValAlaProLeuProThrIleTyrLysArgGlnLysSerGluLeuSerAspGlyIle 178
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                                                                                                                                                                                    AlaMetLeuValAlaGlyAsnAspArgValGlnAlaValIleThrGlnMetGluGluVal 198
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Query Match:
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US-09-764-864-1594/c
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Patent No. US20020132753A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ23
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SEQ ID NO 1594
LENGTH: 599
TYPE: DNA
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CURRENT FILING DATE: 2001-01-17
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                                                                             GCATCTGGTAACTTTTATATATGGAGACCTTTACGAATTCCA-
                                                                                                     AlaSerAsnPro-----LeuTrpGlnSerArgGlySerThrThrValSerSerGlyGly 74
                                                                                                                                                                                  ATGCACAATTTTGAGGAAGAGTTAACTTGTCCCATATGTTATAGTATTTTTGAAGATCCT 536
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1595
; LENGTH: 599
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-864-1595
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PTZ23
CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
                                                    436 ---CTCAAGTGCCCTAATTGCAGAAGTATTACTGAAATTGCTCCAACTGGCATTGAATCT 380
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Best Local Similarity:
Query Match:
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US-09-764-877-2549
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SOFTWARE: Defortor
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CURRENT FILING DATE: 2001-01-17
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                                       ---CTCAAGTGCCCTAATTGCAGAAGTATTACTGAAATTGCTCCAACTGGCATTGAATCT 220
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Query Match:
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US-09-764-877-2550
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Patent NO. US20020147140A1
GEMERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC005
CURRENT APPLICATION NUMBER: US/09/764,877
CURRENT FILING DATE: 2001-01-17
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2550
LENGTH: 599
TYPE: DNA
                                           164 ---CTCAAGTGCCCTAATTGCAGAAGTATTACTGAAATTGCTCCAACTGGCATTGAATCT 220
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US-09-764-864-46

Sequence 46 Application US/09764864

Patent No. US20020132753A1

GENERAL INFORMATION:
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 46
LENGTH: 625
TYPE: DNA
ORGANISM: Homo sapiens
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CURRENT FILING DATE: 2001-01-17
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PTZ23
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                                         191 ---CTCAAGTGCCCTAATTGCAGAAGTATTACTGAAATTGCTCCAACTGGCATTGAATCT 247
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  95 LeuGlnArgAsnLeuLeuValGluAsnIleIleAspIleTyrLysGlnGluSerSerArg 114
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                                                                              ArgPheArgCysProSerCysArgHisGluValValLeuAspArgHisGlyValTyrGly 94
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC005
FILE REFERENCE: PC005
CURRENT APPLICATION NUMBER: US/09/764,877
CURRENT FILING DATE: 2001-01-17
CURRENT FILING DATE: 7001-01-17
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TYPE: DNA
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US-09-250-883-14
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Colpitts, Tracey
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
TITLE OF INVENTION: FOR DETECTING DISEASE OF THE BREAST
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Becker, Cheryl L
REGISTION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 61
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
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STRANDEDNESS: single
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                                                                                                   61 LeuTrpGlnSerArgGlySerThrThrValSerSerGlyGlyArgPheArgCysProSer 80
                   CysArgHisGluValValLeuAspArgHisGlyValTyr-------GlyLeuGln 96
 TGCAACCAG - -
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RESULT 19
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                                                                                                                             ; OTHER INFORMATION: Incyte ID No. US-09-880-192-41
Best Local Similarity:
                      Percent Similarity:
                                                              Pred. No.:
                                                                                Alignment Scores:
                                          score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 41, Application US/09880192 Patent No. US20020077470A1
                                                                                                                                                                                                                                                                                SEQ ID NO 41
                                                                                                                                                                                                                                                                                                                    APPLICANT: Volkmuth, Wayne
APPLICANT: Klingler, Tod M.
APPLICANT: Klingler, Tod M.
APPLICANT: Azimzai, Yalda
TITLE OF INVENTION: POLYNUCLEOTIDES ASSOCIATED WITH CARDIAC MUSCLE FUNCTION
FILE REFERENCE: PB-0009-1 CIP
CURRENT APPLICATION UMBER: US/09/880,192
CURRENT FILING DATE: 2001-06-12
NUMBER OF SEQ ID NOS: 62
                                                                                                                                                                                                                                                                                                  SOFTWARE: PERL Program
                                                                                                                                                                                                                                   LENGTH: 34
TYPE: DNA
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                                                                                                                                                                       NAME/KEY: misc_teature
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                                                                                                                                                                                                             ORGANISM: Homo
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DB:
                                                                                                                 Sequence 3, Application US/09927091 Patent No. US20020119541A1 GENERAL INFORMATION:
                                          APPLICANT: KILLARY, ANN APPLICANT: LOTT, STEVE
        APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCCTTTGTTAGTGAGATAGAATCCTTTTTTAATACCATTGAGGAAAACTGTAGTAAAAAT 1335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTAAAGGTTCAATTAGCAGAATTTCTAGAAAATTTACAAGAAAAGTCCTTGAGGATTGAA 1275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SerMetGluGlnPheSerValSerValGluHisValAlaGluMetLeuArgThrIleAsp 327
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CHANDLER, DAWN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Human US-09-927-091-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: UTSC:651US
CURRENT APPLICATION NUMBER: US/09/927,091
CURRENT FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 60/227,560
PRIOR FILING DATE: 2000-08-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/225,033 PRIOR FILING DATE: 2000-08-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: THE TUMOR SUPPRESSOR CAR-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 3826
TYPE: DNA
1195 GAGGAGCTGGAGGCGGACACGGCCCGCACGCTGACCGACATCGAGCAGAAAGTCCAGCGC
                                                                                                                                                                                                                                                1018
                                     233 GlnAlaLeuAlaArgGluGlnGluGluLysLeuGlnArgValArgGlyLeuIleArgGln
                                                                                                                     213 LeuAsnGlnArgPheGluThrLeuCysAlaValLeuGluGluArgLysGlyGluLeuLeu
                                                                                                                                                                                                                                                                           174 LeuSerAspGlyIle---AlaMetLeuValAlaGlyAsnAspArgValGlnAlaValIle 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59
                                                                             ATCGGCGAGGCCTTCGAGCGGCTGCACCGGCTGCTGCGTGAACGCCAGAAGGCCCATGCTA 1194
                                                                                                                                                             CTGCTCAAGCGACAACTGGCGGAGACC---AAGTCTTCCACCAAGAGCCTGCGGACCACT 1134
                                                                                                                                                                                                 ThrGlnMetGluGluValCysGlnThrIleGluAspAsnSerArgArgGlnLysGlnLeu
                                                                                                                                                                                                                                           CTGCACGAGCAGCATCAGGTCACCGGCATCGACGACGCCTTCGACGAGCTGCAGAGGGAG
                                                                                                                                                                                                                                                                                                                                                               AlaHisLysAspCysGluValAlaProLeuProThrIleTyrLysArgGlnLysSerGlu 173
                                                                                                                                                                                                                                                                                                                                                                                                       GTCAAGCTCTTCTGCCTCACGGACCGCGCGCGTTCTCTGCTTCTTCTGCGACGAGCCTGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                           IleAsnIleTyrCysLeuSerCysGluValProThrCysSerLeuCysLysValPheGly 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATCCTCAACGCGCGCGCGCGCGCGA-----CCCTGCCAGGCGCAC-----GACAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTCAAGCTGGCCAACATCGTGGAGCGCTAC-----AGCTCCTTCCCGCTGGACGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LeuLeuValGluAsnIleIleAspIleTyrLysGlnGluSerSerArgProLeuHisAla 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCCGAGTGCCGGCGCACGTTCGCCGAGCCC-------GCGCTGGCGCCCCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ProSerCysArgHisGluValValLeuAspArgHisGlyValTyrGlyLeuGlnArgAsn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AsnProLeuTrpGlnSerArgGlySerThrThrValSerSerGlyGlyArgPheArgCys 78
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Command line parameters:

-MODEL-frame+_p2n.model -DEV=xlh
-Q-/cgn2_1/USPTO_spool/US09908988/runat_26112002_112154_11213/app_query.fasta_1.519
-DB-Issued_Patents_NA -QFMT=fastap -SUFF1X*=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX-blosum62 -TRANS-human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN=0 -ALIGN=20
-MODE-LOCAL -OUTEMT-pto -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER-US0990898_@CGN_1_17_@runat_26112002_11213 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -MAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=7
-NARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=7
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Maximum DB
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1: /cgn2_5/ptodata/

2: /cgn2_6/ptodata/

3: /cgn2_6/ptodata/

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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/BCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/backfiles1.seq:*
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US-08-095-728B-5

PCT-US94-04190-1

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Sequence 37, Appl
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Sequence 17, Appl
Sequence 13, Appli
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Sequence 20, Appl
Sequence 20, Appl
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US-09-908-988B-2 (Alignment Scores: Pred. No.: Score: Percent Similarity Best Local Similar Query Match: DB:	RESULT 1 US-09-484-970B-37 Sequence 37, Applica Patent No. 6426186 GENERAL INFORMATION APPLICANT: Jones, APPLICANT: Walker, APPLICANT: Walker, TITLE OF INVENTION FILE REFERENCE: PI CURRENT APPLICATION CURRENT FILING DATI NUMBER OF SEQ ID NO SOFTWARE: PERL Pro SEQ ID NO 37 LENGTH: 1757 TYPE: DNA ORGANISM: Homo say FEATURE: NAME/KEY: misc_fee OTHER INFORMATION US-09-484-970B-37		13 14 127 15 16 127 17 18 19 122.5 20 122.5 21 122.5 22 23 122.5 24 122.5 25 26 113.5 27 113.5 28 113.5 29 112.5 20 112.5 21 122.5 23 122.5 24 112.5 25 27 113.5 29 114.6 115.6 116.6 117
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TITLE OF INVENTION: No. 6468750el Cell Regulation
TILE REFERENCE: seq
CURRENT APPLICATION NUMBER: US/09/561,989
CURRENT FILING DATE: 2000-04-27
NUMBER OF SEQ ID NOS: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE:
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   GluSerAlaIleGlnSerMetGluGluProGlnMetAlaLeuTyrLeuGlnGlnAlaLys 284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGCCTGGTGCCCCCGGCCCAGGGTCGTGTGAGCCGGAGGCTGAGCCCACGCAAGGTCTCC
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                                                                       GTGGTTCGAGATCAGATCTCTCACTGCACAGTGAAATTGCGCCAGACCACAGGTCTCATG
                                                                                                                                    ArgValArgGlyLeuIleArgGlnTyrGlyAspHisLeuGluGlySerSerLysLeuVal 264
                                                                                                                                                                                                                                                                                                                                                                                                                 AsnSerArgArgGlnLysGlnLeuLeuAsnGlnArgPheGluThrLeuCysAlaValLeu
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RESULT 3
US-08-724-394A-17
                                                                                                                  US-09-908-988B-2 (1-366) x US-08-724-394A-17 (1-2854)
                                                                                                                                                                           Query Match:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                         Alignment Scores:
                                                                                                                                                                                                                                                                                                               US-08-724-394A-17
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                                                                                                                                                                                                                                                 No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 415-576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Thomas, Winston APPLICANT: Tsuchihashi, Zenta APPLICANT: Wolff, Roger K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature LOCATION: 1..2854 /not OTHER INFORMATION: /not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/O FILING DATE: 01-OCT-1996 CLASSIFICATION: 536
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OPERATING SYSTEM: PC-DOS/MS-DOS
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42 CysGlnHisAsnLeuCysArgLysCysAlaAsnAspValPheGlnAlaSerAsnProLeu
                                        55 GAGGAAGCCACCTGCTCCATCTGCCTGAGCCTGATGACGAACCCAGTAAGCATC--
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Lauer, Peter M.
Ruddy, David A.
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Best Local Similarity:
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APPLICANT:
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CURRENT APPLICATION NUMBER: US/09/484,970B
CURRENT FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 172
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TITLE OF INVENTION: BONE REMODELING GENES
FILE REFERENCE: PB-0014 US
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TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                     lyLeuIleArg--
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APPLICANT: MOSS, Joel
APPLICANT: Mishima, Ko
APPLICANT: Nightingale
APPLICANT: Tsuchiya, M
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                                                                                                                                                                                                                                     TELEFAX: 619-23
INFORMATION FOR SEQ
                                                                                                                                                                                                                                   NAME: Fuller, Michael L.
REGISTRATION NUMBER: 36,516
REFERENCE/DOCKET NUMBER: NIHO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-235-8550
TELEPHONE: 619-235-0176
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/0:
FILING DATE: 19930419
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
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                                                         FEATURE:
                                                                          ANTI-SENSE:
                                                                                               MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1840 TAAATGAGTTGGTAGAAGAATACAGACTGACAGTGAAAGAA 1880
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              348 lyAsnAlaGlyLeuGluGluGluArgLeuAspValProGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     277 laLeuTyrLeuGlnGlnAlaLysGluLeuIleAsnLys---ValGlyAlaMetSerLysV
                                                                                                                                                                 TYPE: nucleic acid
                                     NAME/KEY:
                                                                                                                                      TOPOLOGY:
                                                                                                                                                      STRANDEDNESS: single
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Mishima, Koichi
Mishima, Kaichi
Mishima, Maria
Mishtingale, Maria
Mishina, Mikako
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SIXTEENTH
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US	RESULT US-08- Sequ Pate PA PA PA PA	Оу О О О О О О О О О О О О О О О О О О О	О О О О О О	Db Db
CLASSIFICATION: 436 PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/049,473 FILING DATE: 19-APR-1993 ATTORNEY_AGENT INFORMATION: NAME: Fuller, Michael L. REGISTRATION NUMBER: 35,516 REFERENCE/DOCKET NUMBER: 31070 TELECOMMUNICATION INFORMATION: TELECOMMUNICATION: 1: SEQUENCE: 619-235-9176 TYPE: NUCLEIC acid STRANDENIESS: single TOPOLOGY: linear MOLECULE TYPE: cDNA HYPOTHETICAL: NO ANTI-SENSE: NO FEATURE: NAME/KEY: CDS LOCATION: 11725 08-312-648-1	66 ence 1. enc	AlaGlyArgProGluProGlyTyrGluSerMetGluGlnPheSerValSerValGluHis	280 LeuGInGInAlaLysGlu	GCAGAGAATGCCCGGTCATGTATTCGAGCTTATTTTATGATCTACATGAAACTCTGTGT GluGluProGlnMetAlaLeuTyr ::: :: CGTCAAGAAGAATGGCTCTAAGTGTTGATGATGCTCATGTTCGTGAAAAATTGATTTGG

1988B-2 (1-366) x US-08-312-648-1 (1-3312)
PTCCC 138 Inhala 57 PCCGT 213 Inhala 57 PCCGT 213 Inhara 97 PCCGT 213 Inhara 97 PCCGT 324 PAAAA 273 PTGGT 324 PTGGT

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Alignment Scores: Pred. No.:
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                                                                                           ; LOCATION:
PCT-US94-04190-1
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   Percent Similarity:
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                                                                                                                                                                                                                                                                    TELEFAX: 619-235-0176
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3312 base pairs
                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Fuller, Michael L.
REGISTRATION NUMBER: 36,516
REFERENCE/DOCKET NUMBER: NIHO:
TELEFONMUNICATION INFORMATION:
TELEPHONE: 619-235-8550
TELEFAX: 619-235-0176
                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: The Government of the United States of America APPLICANT: as represented by the Secretary, Department APPLICANT: of Health and Human Services
TITLE OF INVENTION: A MAMMALIAN GUANIN NUCLEOTIDE BINDING TITLE OF INVENTION: PROTEIN WITH AN ADP-RYBOSYLATION FACTOR DOMAIN NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: KNOBBE, MARTENS, OLSON AND BEAR STREET: 620 NEWPORT CENTER DRIVE SIXTEENTH FLOOR
                                                                                                                                                                                MOLECULE TYPE: HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/0419
                                                                                                                                                               ANTI-SENSE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1021 CACTGTGAAAAGACTTTGCAGCAGGATGATTGTAGAGTTGTCTTGGCAAAACAGGAAATT 1080
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                                                                                                                                                                                                                       TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 620 NEWPORT CITY: NEWPORT BEACH
                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AlaGlyArgProGluProGlyTyrGluSerMetGluGlnPheSerValSerValGluHis
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                                                                                                                                                                                                                                                       nucleic acid
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 Length:
Matches:
Conservative:
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3312
78
59
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6	TGTTGTTGATGCTCATGTTCGTGAAAATTGATTTG	Db 901
279	luProGlnMetAlaLeu	Qy 272
900	GCAGAGAATGCCCGGTCATGTATTCGAGCTTATTTTTTATGATCTACATGAAACTCTGTGT	Db 841
271	GlnSerMet	Оу 269
4	:::::: CAPATCGTGGAAGATGGAATTGGAATGGCTCACACAGAACATG	Db 781
268	rA.	Qy 260
œ	TCTCAGATTATTCCAGAAAATTAGTTGGAATTG	Db 721
259	spHisLeuGluGl	Qy 254
720	::: CAGAAGCTAATCAGATCCGAG	66
п (AlaArqGluGlnGlnGlnLvsLenGlnArqValArqClvLovTlovrcCl	Qy 234
233 660		0
0	AAACTAGCCG	Db 586
219	leGluAspAsnSerArgArgGlnLysGlnLeuLeuAsnGln	у 20
585	TGCTCTCAG	и
199	lIleThrGlnMetGluGluValC	Qy 181
N	AAACCTCATGAGAAAACT	50
-,	laProLeuProThrIleTyrLysArgGlnLysSerGluLeuSerAspGlyIlea	0у 161
50	AGTGTTCTCAAGTTACTCATTCTACAAAGACATTAGCAAAGCACAGGCGAGTTC	4.4
ה	yshosvalpheGlvAlaHisLvsAspCvsG	Оу 148
44	TCACCTTGCCTCTGTATATTGCACTGTGTGTGCAACTCATTTGT	ω
4	luHisGluAspGluLysIleAsnIleTyrCysLeuSerCysGluVal	Qy 128
384	CAGTATGGAGCTGCAGAAGAATCCCATTGGGATATCTGGAGAGAG	
)	HisalaTusalaCluCluuis	0v 117
116 324	AATTTTG	27
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7	CysProSerCysArgHisGluValValLeuAspArgH TGCCCATTTGATCGACAAGTAACAGACCTAGGTGATT	Db 214
213	CCTCTTCATGGAAGAGCAATCC	, <u>, , , , , , , , , , , , , , , , , , </u>
77	SerAsnProLeuTrpGlnSerArgGlySerThrThrValSerSerGlyGlyAr	, o Ui
189	CGTCTTTTGCTTTGTGGCCATACCGTCTG	Db 139
57	ValIleLeuProCysGlnHisAsnLeuCysArgLysCysAlaAsnAs	Ωу 38
138	AAGGTGCTAGAGTGTGGAAGTTTGTGAAGATGTCTTTTCTTTGCAAGG	Db 79
37	LysGlnLeuIleCysProIleCysLeuGluMetpheSer	Qy 22
	8-988B-2 (1-366) x PCT-US94-04190-1 (1-3312)	us-09-90
	tch: 19.74% Mismatches: 115 tch: 149 tch: 5 Gaps: 17	Query Mar
	Cimilarit 10 Age	100

Align Pred. Score	RESUI US-08 VS-08 Patal GH IN	Db '	γQ	Db 2	0γ	Db	Qy	DЬ	Qy
Alignment Scores: Pred. No.: Score:	JI 8 JI 095-728B-5 Juence 5, Appleent No. 58438 NERAL INFORM APPLICANT: PAPPLICANT: PAPPLICANT: PAPPLICANT: PAPPLICANT: PAPPLICANT: PAPPLICANT: PAPPLICANT: PAPPLICANT: PAPPLICANT: PAPPLICATE: NEW STATE: NEW COUNTRY: UZIP: 10036 COMPUTER REAL MEDIUM TYPE COMPUTER: PAPPLICATION FELICATION FILING DATE CURSETWARE: WHIT REGISTRATION FILING DATE CULSETWARE: WHIT REGISTRATION FOR APPLICATION FILING DATE CURSETWARE: SOULCULE TYPE: MAMECALIC SOULCULE TYPE: MAMECALIC SOULCULE TYPE: MAMECALIC SOULCULE TYPE: COATION: OTHER INFOR-O95-728B-5	::: 1 ATT	319 Val 319	ъ ,		1021 CACTGTG	293	961 CTCAGGCA	280 LeuGlnG
2.8e-05 132.00	HAN SON SON SON SON SON SON SON SON SON SO			ACAAGGTTACTGGAAACATTGCAGAAACAGCAGCAGC	AlaGlvArgProGluProGlvTvrGluSerMe	::: CACTGTGAAAAGACTTTGCAGCAGGATGATTGTAGAGTTGTCTTG			LeuGlnGlnAlaLysGlu
Length: Matches:	THE DETECTION THE DETECTION RICAS RICAS 838			CAGCAGCAGCAGTTTACAGA	SerMetGlinGlinDhe	GATTGTAGAGTTGTO			LeuIleAsnLysValGlyAla
2155 87	AND OCYTIC LEUKEMIA (APL)		,	AGTTGCAGATCAC 11	ValServalCluHic 31	::: ::: GCAAAACAGGAAATT 10	sValGluLeu 29	AGCCTGCCTC 10	3ValGlyAla 292

Qy 249 1	Db 1071 G	Оу 248-	Qy 241 G Db 1011 G	Db 951 (Qу 225 G	891	2	Oy 185 A Db 831 G	7	Qу 165 Т	Db 720 1	Qy 148 L	Db 660 C	Qу 135 -	Db 600 G	Оу 134 -	Db 540 G	Qy 122 G	Db 480 G	Оу 106 -	420	Ov 97 A	360	Ov 83 -	Qy 64 S Db 327 -	рь 300 c	Qy 44 H	Qy 24 L Db 243 C	us-09-908-9	Percent Simi Best Local S Query Match: DB:
LeuIleArgGlnTyrG :::	CGCTGGTGCAGAGGA		luLys AGATGGCCAGTCGGC	:::::: CGGGCTCAGGAGCGCGI	luGluArgLysGl	CGCGTGCCGAGA	snSerArgArgGlnLv	snAspArgValGlnA ;; ATAGTGCCTTTGGCG	AGATCCAGCAGCGAC	hrIleTyrLys :::	TCGTGCGCGCTCCTTG	euCysLysValPhe	ACCGCACCCCTACGCT		TGCGTGAGTTCCTGGF		CACACCAGTGGTTCCTC	lnHisLeuMetCysGl	AGTCGGCCGACTTCTG	AspIleTy	i GCGCCTGTC	AsnLeuLeuValG	CTGGCCCCTAGGTG	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	erArgGlySerThrThr	GTGCTC	AsnLeuCysArgLy	.euIleCysProIleCy TGCGCTGCCAGCAATG	88B-2 (1-366) x	nilarity: 33.1 Similarity: 20.9 1: 6.90
lyAspHisLeuGluG :::	TGAAGTGCTACGCCTCGG		TGGGCCGCCTGGATGCTG	AGGCTGTG	nAlaLeu	GGAGCTGATCCGCGAG	sGlnLeuLeuAsnGln	aValIleThrGlnMet GTTCACGCGCAGATG	GAGGAGCTGGAC	nLysSerGluLeuSer :::	ACAGCAGCCACAGTGAGC	-GlyAlaHisLysAsp	GACCAGCATCTA	AsnIleTyrCys	ACGGCACCCGCAAGACC?		CAAGCACGAGGCCCGGCCCC	uGluHisG	GTGCTTTGAGTGCGAGC	rLysGlnGluSerSerAr	 GCAGAT	luAsnIleIle		-HisGluValValLeuA	ValSerSerGlyGlyA ::: GCGTCGGGC	AGGATGCCTGGAG	sCysAlaAsnAspValP 	SLeuGluMetPheSer :::	US-08-095-728B-5	17% Conservati 91% Mismatches 0% Indels: Gaps:
lySerSerLysLe ;;;	ACCAGGAGGTGCT		LeuGlnArg TGCTGCAGCGC	GACGCGCGGTACCA	Al	:: GCGTGCGCCAGGT	ArqPheGluThrLe	GLuGLuValCysGInT CACGCGGCCGTCGGCC	CCATGACGCAG	AspGlyIleAlaMe	TCAAGTG		CGAGGATGTTCCAAGCC	LeuSerCysGluValP	ACCAACAACATCTTCTGC		TAGCAGAGC	sile	AGCTCCTCTGCGC	gProLeuHisAl	SCAGGCTGTGTG		 ATAACGTCTTT	\spArqHisGlyValTy	ArgPheArgCysPro ::: ATGCAGTGCCCC		^{>} heGlnAlaSerAsnP	ysProValVa AGTGCCCGAA	(1-2155)	rvative: 51 ltches: 154 .s: 124
:uValGluSerAla :::::::	GGACATGCACG	Gly	ValArg ::: ATCCGCACGGGCAGC	AGCGCGACTACGAG	aArgG	GGTAGCTCACGT	uCysAlaValLeu	GENTATILEGIUASP ::: GGCCAGCTGGGCCGC	GCAGGAGCA	tLeuValAlaGly	CAGCGCA	1A1	GCTG	lProThrCysSer	CTCCAACCCCAAC	1	TGCGCAACCAGTCG		AAGTGCTTCG	aLysAlaGlu	CACCCGCTGCAAA		GAGTCTGCA	rGlyLeuG	SerCysArg ::: ATCTGCCAGGCG		1ProLeuTrpGln	llleLeuProCysGln ::: GCTGCTGCCTTGTCTG		
267	1130	248	247 1070	1010	240	Ü	224	890	·ω	œ	773	164	719	147	659	134	599	134	539	121	479	105	419	96	82 359	326	63	43 299		

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RESULT 9
PCT-US92-02320A-5
; Sequence 5, Application PC/TUS9202320A
; GENERAL INFORMATION:
; GENERAL INFORMATION:
    APPLICANT: Sloan-Kettering Institute, For Cancer Research
; APPLICANT: Sloan-Kettering FOR DETECTION AND TREATMENT OF
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Score:
                                         Alignment Scores:
                    Pred. No.:
                                                                                    PCT-US92-02320A-5
                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 675,084
FILING DATE: 22-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 673,838
FILING DATE: 22-MAR-1991
ATTORNEY AGENT INFORMATION:
NAME: WHITE, JOHN P
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 38694-PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 644-0525
TELEFAX: (212) 42523 COOP UI
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2155 Dase pairs
TYPE: nucleic acid
STEADENDEYNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1131 TTCCTGCGCCAGGCGCTCTGCCGCCTGCGCGAGGGCCCCAGAGCCTGCAAGCTGCC 1190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/0232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIONS
COPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: METHODS FOR DETECTION AND TREATMENT OF CANCER NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS: ADDRESSE: COOPER & DUNHAM
STREETER OF INVENTED OF COOPER & DUNHAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1362 --- CAGGTTCAGGCCCTGGGGCTGGAAGCCCAGCCTATGGCTGTG 1406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1191 GTGCGCACCGATGGCTTCGACGAGTTCAAGGTGCGCCTGCAGGACCTCAGCTCTTGCATC 1250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1251 ACCCAG---GGGAAAGATGCAGCTGTATCCAAGAAAGCCAGCCCAGAGGCTGCCAGCACT 1307
                                                                                                                                                  FEATURE: CDS
                                                                                                                                                                                                                   TOPOLOGY: line: MOLECULE TYPE: cl
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  288 AsnLysvalGlyAlaMetSerLysValGluLeuAlaGlyArgProGluProGlyTyrGlu 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           268 IleGlnSerMetGluGluProGlnMetAlaLeuTyrLeuGlnGlnAlaLysGluLeuIle 287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: UZIP: 10112
                                                                                                         LOCATION: 81..1760 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE
                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                CLONE: MYL-1
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                                                                                                                                                                                                                                                                                     single
  2.8e-05
132.00
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  Length:
Matches:
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FILING DAIL.

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/00513
FILING DATE: January 19, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Pattea L.
REGISTRATION NUMBER: 31,284
REGISTRATION NUMBER: ILI109CIP2
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1NFORMATION:
TELEPHONE: (404) 873-8794
; NAME/KEY: misc_feature
; LOCATION: 1..3511
; OTHER INFORMATION: /function= "PML-RAR' DNA Sequence."
US-08-892-747-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 13, Application US/08892747 Patent No. 6057153 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                   TELEFAX: (404) 873-8795 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 3511 base pairs
TYPE: nucleic acid
                                                                                                                                MOLECULE TYPE: HYPOTHETICAL:
                                                                                      ANTI-SENSE: FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/372,556
FILING DATE: January 13, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS: Pabst ADDRESSE: Patrea L. Pabst STREET: 2800 One Atlantic Center STREET: 1201 West Peachtree Street CITY: Atlanta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1362 --- CAGGTTCAGGCCCTGGGGCTGGCTGAAGCCCAGCCTATGGCTGTG 1406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Shaji T. George, Michael Ma, Martina Werner, APPLICANT: Umberto Pace and Allan R. Goldberg TITLE OF INVENTION: Stabilized External Guide Sequences NUMBER OF SEQUENCES: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1251 ACCCAG----GGGAAAGATGCAGCTGTATCCAAGAAAGCCAGCCCAGAGGCTGCCAGCACT 1307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1191 GTGCGCACCGATGGCTTCGACGAGTTCAAGGTGCGCCTGCAGGACCTCAGCTCTTGCATC 1250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               308 SerMetGluGlnPheSerValSerValGluHisValAlaGluMetLeuArgThrIleAsp 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   288 AsnLysValGlyAlaMetSerLysValGluLeuAlaGlyArgProGluProGlyTyrGlu 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       268 IleGlnSerMetGluGluProGlnMetAlaLeuTyrLeuGlnGlnAlaLysGluLeuIle 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE:
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Y: USA
                                                                                                                                                                            linear
                                                                                                                                  NO
                                                                                                                                                                                               single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Release #1.0, Version #1.25
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Gly 248	248	Qy
AGC 1056	CATCCGCACGGGC	Db
247	luLysLeuGlnArgValArg	Qy
Glu 240 GAG 996	225 GluGluArgLysGlyGluLeuLeuGlnAlaLeu	Qу
GIG 936	CGCGAGCGCGTGCGCCAGGTGGTAGC	Db
Leu 224	lnLeuLeuAsnGlnArgPheGluThrLeuCysAlaVal	Qy
ASP 204 CGC 876	185 ASRASPARGVALGIRALAVAILIETHRGINA 185 ASRASPARGVALGIRALAVAILIETHRGINA 187 EATAGTGCCTTTGGCGCGCGCTCACGCGCAGATGCACGCGGCCGTCGGCCAGCTGGGCCAGCTGGGCCAGCTGGGCCAGCTGGGCCAGATGCACGCGGCAGCATGCACGCGCAGATGCACGCGCACGCTCGGCCAGCTGGGCCAGCTGGGCCAGATGCACGCGGCCGCAGCATGGCACGCGCAGCATGCACGCGCACGCTGGGCCAGCTGGGCCAGCTGGGCCAGATGCACGCGGCCGCAGCATGCACGCGCAGCTGGGCCAGCTGGGCCAGCTGGGCCAGCTGGCACGCGGCAGATGCAAGATGCAACGCGGCCAGCTGGGCCAGCTGGGCCAGCTGGCACGCGCAGATGCAAGATGCAACGCGGCCGTCGGCCAGCTGGGCCAGCTGGGCCAGCTGGCACGCGGCCGCAGATGCAGAGATGCAACGCGGCCGCAGCTGGGCCAGCTGGGCCAGCTGGGCCAGCTGGCACAGATGCAACAACAACAACAACAACAACAACAACAACAACAACAA	ОУ
AG 81	GCGACAGGAGGAGCTGGACGCCATGACGCAGGCGCTGCAGGAG	Db
ly 18	65 ThrIleTyrLysArgGlnLysSerGluLeuSerAspGlyIleAlaMetLeuValA	Qy
3CA 759	ດ`~	Дb
Pro 164	aHisLysAspCysGluValAl	Qy
rGC 705	TGCCGAGGATGTTCCAAGCCGCTGTGCT	Db
Ser 147	snIleTyrCysLeuSer	Qy
AAC 645	586 GTGCGTGAGTTCCTGGACGGCACCCGCAAGACCAACAACATCTTCTGCTCCAACCCCA	뫄
134	134	Qy
CG 58	26 GCACACCAGTGGTTCCTCAAGCACGAGGCCCGGCCCCTAGCAGAGCTGCGCAACCAG	Db 47
μ ω	22 GlantiaTowMotCvsGlwGlwHisGlwAspGlwIvsTlp	
52	66 GAGTCGGCCGACTTCTGGGTGCTTTGAGTGCGAGCAGCTCCTCTGCGCCAAGTGC	B 5
lu 121	06AspIleTyrLysGlnGluSerSerArgProLeuHisAlaLysAla	Ov
A 46		dd Y
105	rqAsnLeuLeuValGluAsnIleIle	04
11 AG 405	TAACGTCTTTTTCGAGAGTCTGC	Db
ln 96	euAspArgHisGlyValTyrGlyLeuG	Qy
CG 345	ATGCAGTGCCCCATCTGCCAGG	DЬ
82	erSerGlyGlyArgPheArgCysProSerCysArg-	Qy
312	ACGCTGTGCTCAGGATGCCTGGAG	Дb
ln 63	isAsnLeuCysArgLysCysAlaAsnAspValPheGlnAlaSerAsnProLeuTrpG	Qу
in 43 TG 285	24 LeuIleCysProIleCysLeuGluMetPheSerLysProValValIleLeuProCysG:	Оy
	-908-988B-2 (1-366) x US-08-892-747-13 (1-3511)	us-09
	Ment Scores: 6.14e-05 Length: 3511 No.: 132.00 Matches: 87 int Similarity: 33.17% Conservative: 51 Local Similarity: 20.91% Mismatches: 154 Local Similarity: 6.90% Indels: 124 Gaps: 17	Alignmen Pred. No Score: Percent Best Loc Query Ma DB:

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US-08-724-394A-20
NAME/KEY: misc_feature;
LOCATION: 1.246240;
OTHER INFORMATION: /not
US-08-724-394A-20
                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 0179
REFERENCE/DOCKET NUMBER: 0179
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 246240 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 20, Application US/08724394A Patent No. 5872237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/
FILING DATE: 01-0CT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1117 TTCCTGCGCCAGGCGCTCTGCCGCCTGCGCCAGGGGCCCCAGAGCCTGCAAGCTGCC 1176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1237 ACCCAG---GGGAAAGATGCAGCTGTATCCAAGAAAGCCAGCCCAGAGGCTGCCAGCACT 1293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1348 ---CAGGTTCAGGCCCTGGGGCTGGCTGAAGCCCCAGCCTATGGCTGTG 1392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Thomas, Winston
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 587
TITLE OF INVENTION: Sequences and Antibodies Thereto
NUMBER OF SEQUENCES: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      328 PheGlnProGlyAlaAlaGlyAspGluGluAspAspAspMetAlaLeu 343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           249 LeuIleArgGlnTyrGlyAspHisLeu---GluGlySerSerLysLeuValGluSerAla 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            288 ASnLysValGlyAlaMetSerLysValGluLeuAlaGlyArgProGluProGlyTyrGlu 307
                                                                                                          MOLECULE TYPE:
                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: Two Embarca
CITY: San Francisco
STATE: CA
                                                                                                                                 STRANDEDNESS:
TOPOLOGY: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                        TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SerMetGluGlnPheSerValSerValGluHisValAlaGluMetLeuArgThrIleAsp 327
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                       /note= "HLA-H.CONTIG"
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US-08-724-394A-21
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CLASSIFICATION: 536
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Feder, John N.
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ADDRESSEE: TOWNSEND and CREW LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Megabase Transcript Map: No. 58 TITLE OF INVENTION: Sequences and Antibodies Thereto NUMBER OF SEQUENCES: 31
                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
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                                                                                                                      APPLICATION NUMBER: US/O FILING DATE: 01-OCT-1996
                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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US-08-724-394A-22
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                                                                                                                                                                                                                                                                                     Patent No. 5872237
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                            Sequence 22,
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                                                                         APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 58
TITLE OF INVENTION: Sequences and Antibodies Thereto
NUMBER OF SEQUENCES: 31
                                                          CORRESPONDENCE ADDRESS:
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LOCATION: 1..246240
OTHER INFORMATION: /note= "HLA-H.CONTIG"
STREET:
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                 ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP STREET: Two Embarcadero Center, 8th Floor
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San Francisco
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Lauer, Peter M.
Ruddy, David A.
Thomas, Winston
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Best Local Similarity:
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INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
                                                                     72057 GGGCAGCTCATCTGCTGGCGCTGTGAGCGGGCACCACAACAAA 72101
                                                                                                                                               72000 CAAGAAATGTCATGTGAGGAACAC---GGAGAGCAGTTCCACCTGTTCTGCGAAGACGAG 72056
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REFERENCE/DOCKET NUMBER: 017
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
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NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                         142 GluValProThrCysSerLeuCysLysValPheGlyAlaHisLys 156
                                                                                                                                                                   122 GlnHisLeuMetCysGluGluHisGluAspGluLysIleAsnIleTyrCysLeuSerCys 141
                                                                                                                                                                                                                                                             102 GluAsnIleIleAspIleTyrLysGlnGluSerSerArgProLeuHisAlaLysAlaGlu 121
                                                                                                                                                                                                                                                                                                                                     82 ArgHisGluValValLeuAspArgHisGlyValTyrGlyLeuGlnArgAsnLeuLeuVal 101
                                                                                                                                                                                                                                                                                                                                                                                                                 62 TrpGlnSerArgGlySerThrThrValSerSerGlyGlyArgPheArgCysProSerCys 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42 CysGlnHisAsnLeuCysArgLysCysAlaAsnAspValPheGlnAlaSerAsnProLeu 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 LysGlnLeuIleCysProIleCysLeuGluMetPheSerLysProValValIleLeuPro 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature LOCATION: 1..246240 OTHER INFORMATION: /no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: not relevant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Indels:
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                               Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LOCATION:
US-07-903-466-2
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 1767 base pairs
TYPE: NUCLEIC ACID
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lauder Leona L.
REGISTRATION NUMBER: 30,86
REFERENCE/DOCKET NUMBER: 9
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TELEFAX: 415-543-4219
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TITLE OF INVENTION: Gene for Ataxia Telangiectasi
TITLE OF INVENTION: Complmentation Group D (ATDC)
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
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648 CATCCGGGACTTTGAGGCCCGCAAGTGT-----CCCGTGCATGGCAAGACG-----
                              103 nIleIleAspIleTyrLysGlnGluSerSerArgProLeuHisAlaLysAlaGluGlnHi 123
                                                                                                                                 574 GCCTCCTTCTGCGAGCTGCATCTCAAGCCCCACCTGGAGGGCGCCGCCCTTC-CGAGACCA 632
                                                                                                                                                                                                                          46 LeuCysArgLysCysAlaAsnAspValPheGlnAla-SerAsnProLeuTrpGlnSerAr
                                                                                                 83 sGluValValLeuAspArgHisGlyValTyrGlyLeuGlnArgAsnLeuLeuValGluAs 103
                                                                                                                                                                   65 g---GlySerThrThrValSerSerGlyGlyArgPheArgCysProSerCysArg---Hi 83
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Matches:
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GENERAL INFORMATION:
APPLICANT: The Regents of the Uni-
                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC
FILING DATE: 19930618
                                                                                                                                                                                                                                                                                                        APPLICANT: The Regents of the University of California TITLE OF INVENTION: Gene for Ataxia-Telangicotasia TITLE OF INVENTION: Complementation Group D (ATDC) NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 177 Post Street, Suite 800
                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1266 CCACGTTGAGAAGATGTGCAAG 1287
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                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1047
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                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
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                                                                                                                                                                                                                                                                     STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          183 aGlyAsnAspArgValGlnAlaValIleThrGlnMetGluGluValCysGln----- 200
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  APPLICATION NUMBER:
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Best Local Similarity:
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236 aArgGluGluGluLysLeuGlnArgValArgGlyLeuIleArgGlnTyrGlyAspHi 256
                                   939 CTTCCGGGACCTGGTGCGGGACCTGGAGAAGCAAAAGGAGGAAGTGAGGGCTGCGCTGGA 998
                                                                     216 gPheGluThrLeuCysAlaValLeuGluGluArgLysGlyGluLeuLeuGlnAlaLeuAl 236
                                                                                                           879 GAAGGAGAAGGACCGCATCAAGAGCTTCACCACCAATGAGAAGGCCATCCTGGAGCAGAA 938
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LENGTH: 1767 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                              694 -----ATGGAGCTCTTCTGCCAGACCGACCAGAC 722
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REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX:
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                                                                                                                                             -----ThrIleGluAspAsnSerArgArgGlnLysGlnLeuLeuAsnGlnAr 216
                                                                                                                                                                                  GCAAAAGGAGCAGCTGCAGCTCAAGATCATTGAGATTGAGGATGAAGCTGAGAAGTGGCA 878
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Indels:
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		One Market One #1.25		NUTION: Complmentation UENCES: 45 E ADDRESS: Leona L. Lauder ewart Street Tower, 18 aza ffrancisco ifornia an Francisco compatible ryTEM: PC-DOS/MS-DOS PATENTIN Release #1.0, CATION DATA: INUMBER: US/07/903,46 : 19920622 TON: 435 TON: 435 TON: 435 TON: 435 TON: 1920622 TON: 435 TON: 192062 TON: 192	TITION: ADDRE Leona Leon	NUMBER OF ENVENTION NUMBER OF SEQUENCE CORRESPONDENCE ADD ADDRESSEE: Leon STREET: Stewart STREET: Plaza CITY: San Franc STAYE: Californ COUNTRY: San Franc STAYE: Californ COUNTRY: San Franc STAYE: San Franc CONTUTER READABLE COMPUTER READABLE COMPUTER: IBM FOPERATING SYSTEM COMPUTER: IBM FOPERATING SYSTEM COMPUTER: LAUGHT INF COMPUTER: LAUGHT INF ATTORNEY/AGENT INF NAME: LAUGHT INF REGISTRATION NUMBER SEQUENCE CHARACTEE TELECOMMUNICATION TELEPHONE: 415-54 REGISTRATION FOR SEQUENCE CHARACTEE LENGTH: 3018 be TYPE: NUCLEIC & STRANDEDNESS: STRANDEDNESS: STRANDEDNESS: STRANDEDNESS: Inf MOLECULE TYPE: OI ANTI-SENSE: NO O7-903-466-1	TITLE (NUMBER CORRESS, ADDRI STREI FILI FILI FILI FILI FILI FILI FILI FI	
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317 1265	SerValSerValGl ::: ::: AATGTATGCATGCG	Ser ::: GACCTGCTCAAT	SerValSerMetGluGlnPheSerValSerValGl ::: ::: GAGGGCCTGGGACAGTCACTAGGCAACTTCAAGGACGACCTGCTCAATGTATGCATGC	GluSerMetGluGlnPhe- ::: ::: CAGTCACTAGGCAACTTCA	CCTGGGACAG	ດ ,	307 1206	ФР
306 1205	CTGCTGGAGGG	GlyTyrA ACCTATCATGTC	aMetSerLysValGluLeuAlaGlyArgProGluProGlyTyr	LeuAlaGl TCTCTCCC	rLysValGlu GAGCAATTAC		292 1146	Qy dd
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273 1106		GlnSerMetGlu ::: CAGACCCGGGAG	SLEUGlUGlySerSerLysLeuValGluSerAlaIleGlnSerMetGluGlu	LysLeuVa ::::: AAGGTGCT	uGlySerSer : ::: rGAGAGAGCC		256 1047	Qу Db
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317 uHisValAlaGluMetLeuArg 324	1270 ATTGATGAGCAATTACTCTCTCCCCCC. 307GluSerMetGluG1:::: :::: 1330 GGAGGGCCTGGGACAGTCACTAGGCAA	292 aMetSerLysValGluLeuAlaGlyAr	274ProGlnMetAlaLeuTyrLeuGln ::: 1231 CATCAGCGACTCTGTGTTTTTTGGGAG	256 SLeuGluGlySerSerLysLeuValGluSerAla	236 aArgGluGlnGluGluLysLeuGlnAro	216 gPheGluThrLeuCysAlaValLeuGluck	201ThrileGluAspAsnSe	183 aGlyAsnAspArgValGlnAlaValIle	163 uProThrIleTyrLysArgGlnLysSei : ::::::::: 904 GGAGGAGGCCAAGGCCGAGAAGGAGACC	143 lProThrCysSerLeuCysLysValPhe(123 sLeuMetCysGluGluHisGluAspGlu	103 nIleIleAspIleTyrLysGlnGluSer ::::: 772 CATCCGGGACTTTGAGGCCCGCAAGTGT	83 sGluValValLeuAspArgHisGlyVal ::: 757 CCAG	-GlySerThrThrValSerSerGly ::: 	46 LeuCysArgLysCysAlaAsnAspValP	nt Similarity: 40.91% Local Similarity: 21.43% Match: 6.64% 1
	ACCCCTG nPhe CTTCAAG	OGluProGlyTyr 306	InGlnAlaLysGluLeuIleAsnLysValGlyAl 292 	uSerAlaIleGlnSerMetGluGlu 273	rgValArgGlyLeuIleArgGlnTyrGlyAspHi 256 ::: ::: :AAGTGAAGGTGATCATGGATGC 1170	ILEUGluGluArgLysGlyGluLeuLeuGlnAlaLeuAl 236	SerArgArgGlnLysGlnLeuLeuAsnGlnAr 216 :::	eThrGlnMetGluGluValCysGln 200 ::::: ::: CATTGAGATTGAGGATGAAGCTGAGAAGTGGCA 1002	rGluLeuSerAspGlyIleAlaMetLeuValAl 183 : :GGAGCTGTCA	SGlyAlaHisLysAspCysGluValAlaProLe 163 	.uLysIleAsnIleTyrCysLeuSerCysGluVa 143 .:::::::: :::ATGGAGCTCTTCTGCCAGACCGACCAGAC 846	SerArgProLeuHisAlaLysAlaGluGlnHi 123	TyrGlyLeuGlnArgAsnLeuLeuValGluAs 103	yGlyArgPheArgCysProSerCysArgHi 83 	<pre>PValPheGlnAla-SerAsnProLeuTrpGlnSerAr 65 :::: ::: CAAGCAGAAGGCGGTCAAGTCCTGCCTGGTGTGCCAG 697</pre>	Conservative: 60 Mismatches: 104 Indels: 79 Gaps: 13 66-1 (1-3018)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
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INFORMATION FOR SEQ ID NO: 1:
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FILING DATE: 19930618
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 22-JUN-199
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ANTI-SENSE:
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LENGTH: 3018 base pair
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REFERENCE/DOCKET NUMBER: 91-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-421-4973
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143 lProThrCysSerLeuCysLysValPheGlyAlaHisLysAspCysGluValAlaProLe 163
                                                                                                                                       103 nIleIleAspIleTyrLysGlnGluSerSerArgProLeuHisAlaLysAlaGluGlnHi 123
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                  sLeuMetCysGluGluHisGluAspGluLysIleAsnIleTyrCysLeuSerCysGluVa 143
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                                                                                                                                                                                                                                                GCCTCCTTCTGCGAGCTGCATCTCAAGCCCCACCTGGAGGGCGCCGCCTTC-CGAGACCA
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177 Post Street, Suite 800
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Conservative:
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                                    -ATGGAGCTCTTCTGCCAGACCGACCAGAC 846
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                       CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: SCOTT, ROBERT E.

TITLE OF INVENTION: CDNA ENCODING P2P PROTEINS AND USE OF
TITLE OF INVENTION: P2P CDNA-DERIVED ANTIBODIES AND ANTISENSE REAGENTS
TITLE OF INVENTION: DETERMINING THE PROLIFERATIVE POTENTIAL OF NORMAL,
TITLE OF INVENTION: ABNORMAL AND CANCER CELLS IN ANIMALS AND HUMANS
                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1063 CTTCCGGGACCTGGTGCGGGACCTGGAGAAGCAAAAGGAAAGGAAGTGAGGGCTGCGCTGGA 1122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          317 uHisValAlaGluMetLeuArg 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                256 sLeuGluGlySerSerLysLeuValGluSerAlaIleGlnSerMetGluGlu------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      236 aArgGluGluGluLysLeuGlnArgValArgGlyLeuIleArgGlnTyrGlyAspHi 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            216 gPheGluThrLeuCysAlaValLeuGluGluArgLysGlyGluLeuLeuGlnAlaLeuAl 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         904 GGAGGAGGCCAAGGCCGAGAAGGAGACGGAGCTGTCA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          163
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                                                                                        APPLICATION NUMBER: FILING DATE: 18-FE
                                                                                                                                                                                                                                                                                                                STREET: 230 COTTY: Philadelphia
  REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                         COUNTRY:
                           NAME:
                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAAGGAGAAGGACCGCATCAAGAGCTTCACCACCAATGAGAAGGCCATCCTGGAGCAGAA 1062
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aGlyAsnAspArgValGlnAlaValIleThrGlnMetGluGluValCysGln------
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                                                                                                                                                                                                                                                                         19102
                         Weiser,
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230 S. Fifteenth Street, Su
                                                                                                                                                                                                                                                                                              USA
                                                                                        18-FEB-1997
Gerard J.
UMBER: 19,763
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                                                                                                                                                                                                                                                                                                                                                                                                                                              ABNORMAL AND CANCER CELLS IN ANIMALS AND HUMANS
                                                                                                             US/08/801,308
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 37
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
TELEFAX: 215-875-8394
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: cDNA
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                   230
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                                                                                                                                                                                                                                                                                                                                                          649 GTAGTATTCAGGTACACTGTCTCG------CCTACCTGCTCCGATACTAAGACAGCA 699
                                                                                                                                                                                                                                                                                                                                                                                               133
                                                                                                                                                                                                                                                                                                                                                                                                                                      595 CAGCGGAACCTACAGCCTCGTAGTAGATCTCCAATACTA-----AGACAGCAGGATCCT 648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       113 SerArgProLeuHisAlaLysAlaGluGlnHisLeuMetCysGluGluHisGluAspGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    475 GCCAACAAGTTTTTACGACAGGCTGTTAATAACTTTAAAAATGAAACTGGCTATACAAAA 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      295 GATCCTATCCCAGCAGAGCTCTTGTGCCTCATCTGCAAAGACATCATGACTGATGCTGTG 354
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TYPE: n
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18 AspAsnLeuGluLysGlnLeuIleCysProIleCysLeuGluMetPheSerLysProVal 37
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                                                                                                                                                                                                                                       GlnLysSerGluLeuSerAspGlyIleAlaMetLeuValAlaGlyAsnAspArgValGln 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ArgAsnLeuLeuValGluAsnIleIleAspIleTyrLysGlnGlu----
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GluLeuLeuGlnAlaLeuAlaArgGluGlnGluGluLysLeuGlnArgValArgGlyLeu 249
                                                                                                                                                                                                                                                                                                                                                                                             LysIleAsnIleTyrCysLeuSerCysGluValProThrCysSerLeuCysLysValPhe 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGACTACGAAAACAGTTACCTCCATTTTTATTTTTAGTACCACCACCAAGACCACTCAGT 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGTCCAACATGTCACCAAAATGATGTTTCTCCTGAT------GCTTTAATT 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CysProSerCys---ArgHisGluValValLeuAspArgHisGlyValTyrGlyLeuGln 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SerAsnProLeuTrpGlnSerArgGlySerThrThrValSerSerGlyGlyArgPheArg
                                                      AAATCG---
                                                                                                                                                                                                        ACTTCTAATCAGTCTTCC-----TTGGCCCCCTCCTGTGTCTGGAAATCCG-----TCT 807
                                                                                         LysGlnLeuLeuAsnGlnArgPheGluThrLeuCysAlaValLeuGluGluArgLysGly 229
                                                                                                                              TCTGCTCCAGCTCCAGTACCTGATATAACTGCAACCGTGTCTATATCAGTCCACTCAGAA
                                                                                                                                                                     AlaValIleThrGlnMetGluGluValCysGlnThrIleGluAspAsnSerArgArgGln
                                                                                                                                                                                                                                                                                GGATCCTGTAGTGATTCAGGTACACTGTCTCGCCTACCTGCTCCGTCTATATCTTCATTA 759
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Matches:
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Indels:
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                                                                                                                   ; LOCATION:
US-08-697-610-1
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Best Local Similarity:
                      Percent Similarity:
                                                            Pred. No.:
                                                                             Alignment Scores:
                                          score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/08697610 Patent No. 6172187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                              TELEFAX: (619) 535-89. INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: CD40 Associated Proteins NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS: ADDRESS: Campbell and Flores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Reed, John C. APPLICANT: Sato, Takaaki
                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1147 CCACCACAGCAAATTAGAAGA 1167
                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1030 TCATTATTACATGGACAGTTGATTCCCACAACTGGCCCAGTA---AGAATCAATGCTGCT 1086
                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                               LENGTH: 2240 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                         NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 1203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 4370 La
CITY: San Diego
                                                                                                                                                          NAME/KEY:
                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGTCCAGGTGGTGGCCGGCCAGGCTGGGAGCATTCCAACAAGCTTGGGTACCTAGTTTCT 1146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----GATGGACCTTTTCGGGATTCTGATAATAATTATTGCCAGCTGCCGCCCTT 924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----GlyArgProGluProGlyTyrGluSerMetGluGlnPheSerValSerValGlu 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ala-----LysGluLeuIleAsnLysValGlyAlaMetSerLysValGluLeuAla 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IleArgGlnTyrGlyAspHisLeuGluGlySerSerLysLeuValGluSerAlaIleGln 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4370 La Jolla Village Drive,
                                                                                                                                                                                                                                                                                                                    (619) 535-8949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Floppy disk
0.000378
122.50
34.47%
21.03%
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                                    Length:
Matches:
    Mismatches:
                      Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Suite
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Qy Db 1	Qy Db 1	Qy Db 1		Db Db	Db Db		Дb	Оy	Дb	Qγ	Db	g Bb	Qy	Qy	Оy	ОУ	Qy	ОУ	US-09	Query DB:
284) 124 (264 1	010	62	02	42	75 82	ν ω	62	02	144	560	νω	117	9 7 458	80 404	392	40 332	20 275	-908	Mat
LysGluLeuIleA ::: GAGTCCCTCCAGA	ValGluSerAlaI ::: ATCCGGTCCTTCC	GlnArgValArgG ::::: CTTCATTTACAGC	euc AAA	SerArgArgGlnL AGTGTAGAAAAAA	AACCTGCTGAAGG	GCG	Cysc GACTGTCCCTGCC	hrcyss CATGCA	AGGTCTTGAGG		HisGluAspGluLy ::: CATTTTGAAGAA	 GGTTGTGC!		ArgAsnLeuLeuVa ::: AGAGAAATTCTGGC	SerCysArgHisGlu' ::: ::: GCGTGTCAAGAGAGC	ProLeuTrpGlnS	euProCys	euGluLys :: TGGAGGAC	-988B-2 (1-36	ch:
snLysValGlyAla ::: ACCGCGTGACCGAG	leGlnSerMetGlu ::: GGCAGAACTGGGAG	lyLeuIleArgGlr ::: GAGTGATAGACAGC	euGluGluArgLySGlyGluLeuLeuG ::: AAATTGAGAGACAAAAGGAAATGCTT-	xgGlnLysGlnLeuLeuAsr ::: hAAAAAAACAAGAGCATACA	IleThrGlnMetc ::: AGTGGAGCAACTCGCTCC	laMetLeuValAla ;;; ACCAGCAGATCAA(CysGluValAlaProLeuProThrI CTGCGTGGTGGTGTCCTGCCCTCACA	:CysLys :TGCAAGAGTCAGGT	AAGACCTGCGAC	1 1 1 1 1 1 1 1	sIleAsnIl	 GCAGTTAAC	D	lGluAsnIleI : rC	ValValLeu ::: ATCGTTAAA	erArgGlySerTh	isasnLeuCysar 	lnLeuIleCysProIl :: \GTACAAGTGTGAGAA	6) x US-08-697	6.418 4
AsnLysValGlyAlaMetSerLysValGlu ::: AlcGCGCTGACCGAGCTGGAGAGCGTGGAC	ValGluSerAlaIleGlnSerMetGluGluProGlnMetAla :::	rgValArgGlyLeuIleArgGlnTyrGlyAspHisLeuGluGlySerS 	lnAlaLeuAl	SnGlnArgPheGluThrLeuCysAla ::: ::: AAAGTTTGCACAATCAGATATGTAGC	luGlu ::: AAAAG	\snAspAr :::::: CACGAGGC	ProThrIleTyrLysArgGln CCTCACAAGTGCAGCGTCCAG	i i	CACGTGGAGAAGGC		ı Ö	GGGACATCTGCTGGT		leaspIleTyrLysGl :: :TTCAGATCTATTGTCG	ArgHisGlyVal] ::: AAGGTGT	hrval	yscys GCTGC	IleCysLeuGluMetPhes aAGTGCCACCTGGTGCTG	-610-1 (1-2240)	Indels: Gaps:
LeuAlaGlyArgPro ::: AAGAGCGCGGGGCAAGTG	LeuTyrLeuGlnGlnAla	IGluGlySerSerLysLeu ::: AAGGAGCTTGACAAGGAG	aArgGluGlnGluGluLySLeu ::: -CGAAATAATGAATCCAAAATC	rLeuCysAlaVal ::: ::: :ATATGTAGCTTTGAAATT	ValCysGlnThrIleGluAspAsn ::::::: AAGGTTTCCTTGTTGCAGAATGAA	gValGlnAlaVal cagcTccgccgTgcAgcAcgTc	sArgGlnLysSerGluLeu CGTCCAGACTCTCCTGAGG	-ValPheGlyAlaHisLysAsp ::: CGCGCTGCAGAAACACGAAGACACC	GTGTAAATACCGGGAAGCC		uValPro GCGTCCTGACTGCAAAGAA	AAAATGATT	ıMetCysGluGl	3lnGluSerSerArgProLeu ::: 	YrGlyLeuGln :: TTAAGGATAATTGCTGCAAG	.yGlyArgPheArgCysPro ::: AAATGTACA	AlaAsnAspValPheGlnAlaSerAsn 	eSerLysProValValIle GTGCAGCCCGAAGCAG		109 19
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Вb
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; LOCATION:
US-08-349-357-1
                                                                                                                            Query Match:
                                                                                                                                        Percent Similarity:
Best Local Similarity:
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US-08-349-357-1
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                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (619) 535-894
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/349,357
FILING DATE: 02-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 1203
                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Reed, John C.
APPLICANT: Sato, Takaaki
TITLE OF INVENTION: CD40 Associated Proteins
NUMBER OF SEQUENCES: 17
275 GTGGAGGACAAGTACAAGTGTGAGAAGTGCCACCTGGTGCTGCTGCAGCCCGAAGCAG--- 331
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STATE: California
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TYPE: nucleic acid
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4370 La Jolla Village Drive, Suite 700
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Indels:
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Matches:
Conservative:
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Db Qy

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В Qy g 9

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Вр
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Search completed: December 3, 2002, 14:17:02
Job time : $384\ \text{secs}$

Вþ

OM protein - nucleic search, using frame_plus_p2n model

December 3, 2002, 12:12:18; Search time 261 Seconds (without alignments) 3157.975 Million cell updates/sec

Perfect score: US-09-908-988B-2
1912
1 MNFTYGFKPLLGDAHNMDNL.....EGNAGLEEERLDVPEGSGLH 366

Scoring table:

Xgapop 10.0, Ygapop 10.0, Fgapop 6.0, Delop 6.0, Xgapext Ygapext Fgapext Delext 7700

2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Command line parameters:

-MODEL-frame+_p2n.model -DEV=xlh
-O-/cgn2_1/USPTO_Spool/US09908988/runat_26112002_112153_11206/app_query.fasta_1.519
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-DB=N_Geneseq_101002 -OFMT=fastap -SUFFIX=ring -MINMANCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -MATRIX-blosum62 -TRANS-human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN=0 -ALIGN=20
-MODE=-LOCAL -OUTFMT=pto -NORM-ext -HEAPSIZE=500 -MINLEN=2=0 -MAXLEN=2000000000
-USER=-US0990898_eCGN_1_1_0_erunat_26112002_112153_11206 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XCARPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7

YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

N Geneseg 101002 : /SIDS2/gcgdata/geneseq/geneseqn-emb1/WA1986_DAT: *
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10: 111: 113: 114: 115: 116: 117: 118: 119: 120: 221:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

Query

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2058 2237 6630 650 391 2276 6768 6768 6768 6768 11755 11755 2566 1276 1276 1276 3262 3262 298 3262 298	1431 1993 1990 1349 21500 1500 1500 1502 1502 1702 1702 1703 1703 1703 1703 1704 1704 1704 1704 1704 1704 1704 1704	Length
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AAS82247 AAS82248 AAK52236 AAC75760 AAC75769 AAC75769 AAS44635 ABQ91959 AAF158617 ABV51565 ABV5165 ABV5165 ABW5165 ABW5165 ABW72500 AAF158165 ABW72500 AAF158165 ABW72500 AAF17707 AAL36185	ABA99061 AAH78026 AAA77443 AAH78026 AAA77443 AAN83313 AAF27653 AAS25855 AAA99063 AAA825885 AAA82449 AAA825885 AAA825881058 AAA82581058 AAA82581058 AAA82581058 AAA82581058 AAA82581058 AAA82581058 AAA82681058 AAA82688 AAA82688 AAA82688 AAA82688 AAA82688 AAA82688 AAA82688 AAA82688 AAA82688 AAA8268	ID
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ALIGNMENTS

RESULT 1 ABA99061

ABA99061 standard; DNA; 1431

FFH OSS ABA99061;

15-JUL-2002 (first entry)

Murine muscle ring finger protein 1 (MURF-1) coding sequence.

Muscle ring finger; MURF-1; mouse; cardiant; microtubule; intermediate filament; striated muscle; cardiac hypertrophy; heart disease; gene; ds.

Mus musculus

Location/Qualifiers 199..1299

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                                                                                                                                                                                                                                                                                                                                 Query
                                                                                                                                                                                                                                                                                                                                                                       Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence encodes murine muscle ring finger protein 1 (MURF-1). The cinvention relates to a purified muscle ring finger (MURF) protein, selected from MURF-1, MURF-2 and MURF-3. The MURF proteins of the invention are involved in microtubule and intermediate filament stabilisation of striated muscle cells and have cardiant activity. The MURR proteins are useful for screening a candidate substance for MURR proteins are useful for screening that continues, homodimerisation of MURF-1, MURF-2 or MURF-3 tabilisation of MURF-1, MURF-2 or MURF-3 tabilisation of microtubules, interaction of MURF with intermediate filaments, e.g. desmin, vimentin and cytokeratin, and heterodimerisation of MURF.

The screened compounds are useful for treating and preventing cardiac hypertrophy and heart diseases. MURF proteins are useful as antigens to immunise animals for the production of antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel muscle ring finger protein useful for drug screening, and diagnosing and treating diseases, particularly cardiomyopathies
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
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                                              TGTAGGCACGAGGTTGTCCTGGACAGGCATGGTGTCTATGGCCTGCAGCGGAACCTGCTA
                                                                                                CTGTGGCAATCCCGGGGCTCCACAACGGTGTCTTCAGGAGGACGTTTCCGATGCCCATCT
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06-DEC-1999; 99JP-0346864.
08-FEB-2000; 2000JP-0031062.
10-FEB-2000; 2000JP-0034090.
10-FEB-2000; 2000JP-0034091.
14-FEB-2000; 2000JP-0035829.
14-FEB-2000; 2000JP-0035899.
14-MAR-2000; 2000JP-0071161.
30-MAY-2000; 2000JP-0071161.
                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is a human protein coding sequence. The human protein, preferably originated from tumour cell line, is applicable as a drug, a reagent for studying intracellular protein networks and a protein source for screening proteins for binding low molecular weight drugs. The human protein coding sequence is useful for gene diagnosis and gene therapy, expression vectors and transformant cells for detection of ligands and receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for drug
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CysGluValProThrCysSerLeuCysLysValPheGlyAlaHisLysAspCysGluVal
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                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence encodes a human cardiomyopathy associated protein (CAP) that is differentially expressed in human left ventricle assist device (LVAD) myocardial biopsy samples. The predicted isoelectric point of CAP is approximately 12.2. The CAP polynucleotide and polypeptide are useful for diagnosing, preventing or treating cardiomyopathy. The treatment diminishes the occurrence of at least one of the following symptoms associated with cardiomyopathy: reduced ejection fraction, increased left ventricular wall thickness, increased atrial size, valvular regurgitation, exertional intolerance or ventricular tachyrhythmia. Modulators of CAP are also useful for preventing or treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid encoding a cardiomyopathy associated protein that is differentially expressed in human left ventricle assist device (LVAD) myocardial biopsy samples, useful for diagnosing, preventing or treating cardiomyopathy -
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99US-0117905.
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neuroprotective; cytostatic; gene therapy; gene; ss.
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Best Local Similarity:
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13-FEB-2001;
14-FEB-2001;
23-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is the coding sequence for a human cytoskeleton-associated protein (CSAP). The CSAP and its coding sequence are useful in the diagnosis, treatment and prevention of a cell proliferative disorder such as actinic keratosis, atherosclerosis, psoriasis, primary thrombocythaemia, leukaemia; a viral infection such as those caused by adenoviruses (acute respiratory disease, pneumonia), arenaviruses (lymphocytic choriomeninigitis); and a neurological disorder such as epilepsy, ischaemic cerebrovascular disease, stroke, cerebral neoplasms, Alzheimer's disease, Pick's disease, Huntington's disease or amyotrophic lateral sclerosis. The CSAP coding sequence is also useful for creating knock out or knock in humanised animals or transgenic animals to model human diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    treating ischemic
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                                              CTATGGCAGTCCCGGGGCTCCACCACTGTGTCTTCAGGAGGCCGTTTCCGCTGCCCATCG
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A, Duggan BM, Xu Y, Walia NK, Griffin JA,
R, Khan FA, Thangavelu K, Ison CH, Azimzai
KJ, Lal PG, Sanjanwala MM, Elliott VS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to human transcriptional regulator protein (TXREG) sequences. The antagonist and an agonist of the proteins of the invention are used to treat disorders associated with decreased
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1500 BP; 401 A; 378 C;
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                                                                                                                             Claim
                                                                                                                                                                     Novel muscle ring finger protein useful for drug screening, and diagnosing and treating diseases, particularly cardiomyopathies
                                                                                                                                                                                                                                                                                                                                  Olson
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The sequence encodes murine muscle ring finger protein 2 (MURF-2). invention relates to a purified muscle ring finger (MURF) protein, selected from MURF-1, MURF-2 and MURF-3. The MURF proteins of the

invention are involved in microtubule and intermediate filament

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       e.g. desmin, vimentin and cytokeratin, and heterodimerisation of MURF. The screened compounds are useful for treating and preventing cardiac hypertrophy and heart diseases. MURF proteins are useful as antigens to immunise animals for the production of antibodies.
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                                             TACGGCATCCTGGAGGAGGAAGACTGAAATGACCCAAGCCATCACTCGAACACAGGAG
                                                                          CysAlaValLeuGluGluArgLysGlyGluLeuLeuGlnAlaLeuAlaArgGluGlnGlu
                                                                                                                                    ThrIleGluAspAsnSerArgArgGlnLysGlnLeuLeuAsnGlnArgPheGluThrLeu
                                                                                                                                                                   LeuValAlaGlyAsnAspArgValGlnAlaValIleThrGlnMetGluGluValCysGln
                                                                                                                                                                                                                              GCTCCCCTGACTCATGTGTTCCAGAGGCAGAAGTCAGAGCTCAGTGATGGTATTGCTGTA
                                                                                                                                                                                                                                            AlaProLeuProThrIleTyrLysArgGlnLysSerGluLeuSerAspGlyIleAlaMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGCAGACATGAGGTGGTGATAGACAGACATGGGGTCTATGGACTGCAGAGGAACCTGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TACTTACCCACAAGAGGAGGCACCACCGTGGCATCAGGGGGCCGCTTCCGCTGTCCCTCC
                                                                                                         ACTATTGAGGAGTGCTGCAGAAAGCAGAAACAGGACCTGTGTGAGAAATTTGATCACCTA
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76.99%
61.92%
60.77%
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Matches:
Conservative:
Mismatches:
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Gaps:
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RESULT 8
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07-JUN-2000;
28-JUN-2000;
30-JUN-2000;
07-JUL-2000;
11-JUL-2000;
11-JUL-2000;
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04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; opthalmalogical; vulnerary; secreted protein; rheumatoid arthritis; hyperproliferative disorder; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; cerebral ischaemia; anglogenesis; nervous system disorder; cerebral ischaemia; anglogenesis; ocuparous system disorder; cardiac disorder; cerebral ischaemia; anglogenesis; nervous system disorder; halphalmer's disease; infection; ocular disorder; corneal infection; wound healing; epithelial cell proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1085
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19-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                              16-MAR-2000;
17-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; immunosuppressive; antiarthritic; ss; antirheumatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human cDNA encoding a novel secreted protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAGAATGCCAAGACCCTGTTGCAAAAGATCGTGGAAGCATCAAAGGCGTTTCAGATGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GlnGlnAlaLysGluLeuIleAsnLysValGlyAlaMetSerLysValGluLeuAlaGly 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SerLysLeuValGluSerAlaIleGlnSerMetGluGluProGlnMetAlaLeuTyrLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAGGCAGAAAATGTT 1150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GluGlySerGlyLeu 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCCAAGTTGGTGGAGTCAGGAATCCAGTTCATGGATGAGCCCGAAATGGCAGTATTTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAGAAACTGGAACATGTCCGAACTCTTATCAGGAAGTATTCCGATCACCTGGAGAACGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ageing; food additive; preservative; antiproliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCAGGAGAAATAGATGAAGAAGGAGAAGGA---
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                                                                                                        2000US-0216647.
2000US-0216880.
2000US-0217487.
2000US-0217496.
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                                                                                                                                                                                                                         2000US-0214886
2000US-0215135
                                                                                                                                                                                                                                                                                                                                    2000US-0189874.
2000US-0190076.
2000US-0198123.
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                                                 2000US-0218290
2000US-0220963
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14-AUG-2000; 14-AUG-2000; 14-AUG-2000;

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17-NOV-2000;
17-NOV-2000;
          The invention relates to isolated nucleic acid molecules and their encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunoscorbant assays (ELISA). Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. alzheimer's disease, infections caused by bacteria, viruses and fungi
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08-NOV-2000;
                                                                                                                                                                                                                                               diagnosing, pused as food
                                                                                                                                                                                                                                                                                                     P-PSDB;
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17-NOV-2000;
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17-NOV-2000;
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                                                                                                                                                                                                                    Claim 1;
                                                                                                                                                                                                                                            New nucleic acid molecules encoding 461 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions used as food additives or preservatives -
                                                                                                                                                                                                                                                                                                                     WPI; 2001-488783/53.
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and ocular disorders e.g. corneal infection,
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                                                                                                                                                                                                                                                                                                                                                CA,
                                                                                                                                                                                                                                                                                                      AAU15868.
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2000US-0246523.
2000US-0246525.
2000US-0246526.
2000US-0246528.
2000US-0246611.
2000US-0246611.
2000US-0249207.
2000US-0249217.
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2000US-0251868.
2000US-0251868.
2000US-0251869.
2000US-0251869.
2000US-0251990.
2000US-0251990.
2000US-0251990.
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14-SEP-2000; 14-SEP-2000; 14-SEP-2000;

14-SEP-2000; 14-SEP-2000;

14-SEP-2000; 14-SEP-2000;

2000US-0234997. 2000US-0234998. 2000US-0235484.

2000US-0235834.

2000US-0234223. 2000US-0234274.

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06-SEP-2000; 08-SEP-2000;

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22-AUG-2000; 22-AUG-2000; 22-AUG-2000; 23-AUG-2000; 30-AUG-2000; 01-SEP-2000; 01-SEP-2000; 01-SEP-2000; 01-SEP-2000; 05-SEP-2000; 05-SEP-2000; 06-SEP-2000;

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stabilisation of striated muscle cells and have cardiant activity The MURF proteins are useful for screening a candidate substance for MURF protein-binding activity, in a cell, cell-free system or in vivo, and its effect on interaction of MURF with microtubules, homodimerisation of MURF, MURF-1, MURF-2 or MURF-3 stabilisation
                                                                                                                                                                      The sequence encodes murine muscle ring finger protein 3 (MURF-3) invention relates to a purified muscle ring finger (MURF) protein, selected from MURF-1, MURF-2 and MURF-3. The MURF proteins of the
                                                                                                                                                                                                                                                                                                                                                  Novel muscle ring finger protein useful diagnosing and treating diseases, partic
                                                                                                                                                                                                                                                                                            Claim 4; Page 131-133; 134pp; English.
                                                                                                                                                 invention are involved in microtubule and intermediate filament
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TEXA ) UNIV TEXAS SYSTEM
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                                                                         of microtubules, interaction of MURR with intermediate filaments, e.g. desmin, vimentin and cytokeratin, and heterodimerisation of MURF. The screened compounds are useful for treating and preventing cardiac hypertrophy and heart diseases. MURF proteins are useful as
                                                to immunise animals for the production of antibodies.
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1052 CAGCTGGAAAAGTCCACCAAGCTTGTGGAGACCGCCATCCAGTCCCTGGATGAGCCCGGA 1111
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                                                                                                                                                                                   GluGluValCysGlnThrIleGluAspAsnSerArgArgGlnLysGlnLeuLeuAsnGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ThrValGlyPheLys------ProLeuLeuGlyAspAlaHisAsn
                                                                  AspGlyIleAlaMetLeuValAlaGlyAsnAspArgValGlnAlaValIleThrGlnMet ::: ||||:::|||:::|||:::
                                                                                                                                                                                                                                                                             CAGGCCTGTGAGGTTGCCCCTTTGCAAAGCATCTTCCAAGGACAGAAGACTGAGCTGAGT
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                                                                                                                                                                                                                      AACTGCATCTCCATGCTGGTGGCGGGGAACGACCGAGTGCAGACGATCATCTCTCAGCTG
                                                                                                                                                                                                                                                                                              LysAspCysGluValAlaProLeuProThrIleTyrLysArgGlnLysSerGluLeuSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MetAspAsnLeuGluLysGlnLeuIleCysProIleCysLeuGluMetPheSerLysPro
                          HisLeuGluGlySerSerLysLeuValGluSerAlaIleGlnSerMetGluGluProGln
                                                     ACGCAGGAGCAGGAGAAGCTGGGCTTCATCGAGGCTCTGATCCTCCAGTACAGGGAG
                                                                                                           GAGGACTCGTGCAGAGTGACCAAGGAGAATAGCCACCAGGTGAAGGAGGAGCTGAGTCAG
                                                                                                                                                                                                                                                                                                                                    ATCTACTGTCTCACGTGTGAGGTGCCTACTTGCTCCTTGTGCAAGGTGTTTGGGGCTCAC
                                                                                                                                                                                                                                                                                                                                                            IleTyrCysLeuSerCysGluValProThrCysSerLeuCysLysValPheGlyAlaHis
                                                                                                                                                                                                                                                                                                                                                                                                                   LeuHisAlaLysAlaGluGlnHisLeuMetCysGluGluHisGluAspGluLysIleAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                               AGGAACCTGCTGGTAAAACATCATTGACATCTACAAGCAGGAGTGCTCCAGTCGGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ArgCysProSerCysArgHisGluValValLeuAspArgHisGlyValTyrGlyLeuGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCTGCGAATCCCTACTGGACCAACCGCGGTGGCTCAGTGTCCATGTCTGGAGGTCGTTTC
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                                                                                                                                                                                                                                                                                                                                                                                        -CAGAAAGGCAGCCACCCGATGTGCAAGGAACACGAAGACGAGAAGATCAAC
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58.05%
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Mismatches:
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The invention relates to novel human molecules for disease detection and treatment (mddt proteins) and the polynucleotides encoding them. The MDDT polynucleotides and polypeptides are useful for diagnosti and therapeutic purposes e.g. to diagnose and treat cell proliferative disorders (e.g. arteriosclerosis, cirrhosis and psoriasis) cancers (e.g.

diagnostic

and breast cancer) autoimmune disorders

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Chen A, D'Sa SA, Amshey S, D
Chen GE, Flores V, Fong WT,
Charles V, Rosen F
                                                                                                                                                                                                                                                                                                                                                                                                                           16-MAY-2000;
17-MAY-2000;
17-MAY-2000;
                                                                                                                                             New disease detection and treatment molecule polynucleotides and polypeptides, useful for diagnosis and treatment of arteriosclerocirrhosis, psoriasis, cancer, autoimmune disorders, diabetes mel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  arteriosclerosis; cirrhosis; psoriasis; cancer; adenocarcinoma; leukaemia; breast cancer; autoimmune disorder; AIDS; acquired immunodeficiency syndrome; Addison's disease; diabetes mellitus; asthma; multiple sclerosis; osteoarthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; molecules for disease detection and treatment; mddt; ss; Antiarteriosclerotic; hepatotropic; antipsoriatic; cytostatic; immunosuppressive; antidiabetic; antiasthmatic; neuroprotective; osteopathic; antiarthritic; cell proliferative disorder;
                                                                                                    Claim
                                                                                                                                                                                                                                                              Wright RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1172
                                                                                                                                                                                                                                                                                                                                                    (INCY-)
                                                                                                                                                                                                                                                                                                                                                                                              17-MAY-2000;
17-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGGGCTACCTTCCTCAAGTGCCAAGCAGCTCATCAAGAGCATTGTAGAAGCCTCCAAG
                                                                                                                                                                                                       2001-570631/64.
DB; AAU25438.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MetAlaLeuTyrLeuGlnGlnAlaLysGluLeuIleAsnLysValGlyAlaMetSerLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ValGluHisValAlaGluMetLeuArgThrIleAspPheGlnProGlyAlaAlaGlyAsp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA encoding an mddt protein, clone LG:247384.1:2000MAY19
                                                                                                                                                                                                                                                                                                                                                     INCYTE GENOMICS INC
                                                                                                                                                                                                                                                          R, Spiro PA, Banville SC, Shah P, Chalup MS, Cha
D'Sa SA, Amshey S, Dahl CR, Dam TC, Daniels SE,
E, Flores V, Fong WT, Greenawalt LB, Hillman JL,
Roseberry AM, Rosen BH, Russo FD, Stockdreher TK,
J, Yap PE, M, U, JY, Bradley DL, Bratcher SR, Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard;
                                                                                                                              psoriasis, cancer, autoimmune disorders, multiple sclerosis
                                                                                                                                                                                                                                                Hodgson DM,
                                                                                                                                                                                                                                                                                                                                                                               2000US-0185213.
2000US-0205232.
2000US-0205285.
2000US-0205286.
2000US-0205287.
2000US-0205287.
2000US-0205323.
2000US-0205324.
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                                                                                                                                                                                                                                                Jackson S;
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                                                                                                                                                           of arteriosclerosis,
                                                                                                                                               diabetes mellitus,
                                                                                                                                                                                                                                                                                                                     Chang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (e.g. acquired immunodeficiency syndrome (AIDS) and Addison's disease) diabetes mellitus, asthma, multiple sclerosis, osteoarthritis, and man more diseases given in the specification. The present sequence encodes an mddt protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2110 BP;
917
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                          GlnSerMetGluGluProGlnMetAlaLeuTyrLeuGlnGlnAlaLysGluLeuIleAsn
                                                                                                                                                                                                                                                                                 GlnAlaValIleThrGlnMetGluGluValCysGlnThrIleGluAspAsnSerArgArg
                                                                                                                                                                                                                                                                                                                                                                                                 CysLysValPheGlyAlaHisLysAspCysGluValAlaProLeuProThrIleTyrLys
                                                                                                                                                                                                                                                                                                                                                                                                                                              CACGAAGATGAGAAAATCAACATCTACTGTCTCACGTGTGAGGTGCCCACCTGCTCCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                             HisGluAspGluLysIleAsnIleTyrCysLeuSerCysGluValProThrCysSerLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAGGAGTGCTCCAGTCGGCCGCTG-----CAGAAGGGCAGTCACCCCATGTGCAAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HisGlyValTyrGlyLeuGlnArgAsnLeuLeuValGluAsnIleIleAspIleTyrLys 109
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CAGTCCCTGGACGAGCCTGGGGGGAGCCACCTTCCTCTTGACTGCCAAGCAACTCATCAAA
                                                                                                                                                       GlyGluLeuLeuGlnAlaLeuAlaArgGluGluGluLysLeuGlnArgValArgGly
                                                                                                                                                                                        GTAAAGGAAGAGCCAGAAGTTTGACACGTTGTATGCCATCCTGGATGAGAAGAAA
                                                                                                                                                                                                                    GlnLysGlnLeuLeuAsnGlnArgPheGluThrLeuCysAlaValLeuGluGluArgLys
                                                                                                                                                                                                                                                     CAGACCATCATCACTCAGCTGGAGGATTCCCGTCGAGTGACCAAGGAGAACAGTCACCAG
                                                                                                                                                                                                                                                                                                                    GGACAAAAGACTGAACTGAATAACTGTATCTCCATGCTGGTGGCGGGGAATGACCGTGTG
                                                                                                                                                                                                                                                                                                                                                ArgGlnLysSerGluLeuSerAspGlyIleAlaMetLeuValAlaGlyAsnAspArgVal 188
                                                                                                                                                                                                                                                                                                                                                                               TGCAAGGTGTTTGGGATCCACAAGGCCTGCGAGGTGGCCCCATTGCAGAGTGTCTTCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GlnGlu---SerSerArgProLeuHisAlaLysAlaGluGlnHisLeuMetCysGluGlu 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATGGGGTATATGGACTTCAGAGGAACCTGCTGGTGGAGAACATCATCGACATCTACAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATGGCATCAGGGGGCCGATTCCGCTGCCCATCCTGTAGACATGAAGTGGTTTTTGGATAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGTGCCAATGATATTTTCCAGGCCTCTAACCCGTATTTGCCCACAAGAGGAGGTACCACC
                                                           CTCATCCAGCAGTACCAGGAGCAGCTGGACAAGTCCACAAAGCTGGTGGAAACTGCCATC
                                                                                         LeuIleArgGlnTyrGlyAspHisLeuGluGlySerSerLysLeuValGluSerAlaIle
                                                                                                                         AGTGAGTTGCTGCAGCGGATCACGCAGGAGCAGGAGAAAAAGCTTAGCTTCATCGAGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity:
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78.29%
60.86%
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Matches:
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RESULT 11
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25-APR-2000;
09-JUL-2000;
                                                                                                                                                                                                                      Ford
                                                                                                                                                                                                                                                                                                                                                                                                                                                        antiviral; antibacterial; antifungal; anti-HIV; haemostatic;
immunosuppressive; gene therapy; cytokine cell proliferation;
cell differentiation modulator; immune disorder; infection; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAH90037;
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                                                                                                                                    Novel bone-marrow-expressed polynucleotides and polypeptides, useful for treating e.g. cancer and immune deficiency disorders - \!\!\!\!
                                                                                                                                                                                                  Zhao
                                                                                                                                                                                                                                                                                              03-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                          Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                              human immunodeficiency virus; HIV; autoimmune disorder; haemophilia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human bone marrow cDNA,
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19-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bone marrow; antiinflammatory; cytostatic; neuroprotective;
                                                                                                                                                                                                              Wang
                                                                                                                                                                    AAM00918
                                                                                                                                                                                                                                            HYSEQ INC.
                                                                                                                                                                                                 ang J,
Zhou I
                                                                                                                                                                                                                      Boyle BJ,
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2000US-0552317.

2000US-0598042.

2000US-0620312.

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                                                                                                                                                                                                              Werhman
                                                                                                                                                                                                 Verhman T, Xu Drmanac RT;
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infection, or may result from an autoimmune disorder, a coagulation disorder (e.g. haemophilia), inhibition of tumour cell proliferation, suppression of an inflammatory response or treatment of a nervous system disorder such as Alzheimer's disease. Detection of the presence

increased expression of the polynucleotide or

the protein

presence

expressed in the bone marrow. The polynucleotide and the polypeptide encoded by it are useful in the treatment of various immune deficiencies and disorders. The deficiencies and disorders may be genetic, may be caused by a viral (e.g. HIV), bacterial or fungal

present sequence is one of 251 novel human

polynucleotides

Claim

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Page 397; 648pp; English.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    encodes is useful for the diagnosis and/or prognosis of one or more types of cancer. The polynucleotide and polypeptide can used as nutritional sources or supplements and in the screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1231 BP; 332 A;
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CAGTCCCTGGACGAGCCTGGGGGAGCCACCTTCCTCTTGACTGCCAAGCAACTCATCAAA 1000
                                                                             LeuIleArgGlnTyrGlyAspHisLeuGluGlySerSerLysLeuValGluSerAlaIle
                                                                                                                                          GlyGluLeuLeuGlnAlaLeuAlaArgGluGluGluLysLeuGlnArgValArgGly
                                                                                                                                                                                                          GlnLysGlnLeuLeuAsnGlnArgPheGluThrLeuCysAlaValLeuGluGluArgLys
                                                                                                                                                                                                                                                                                                                                                                                CysLysValPheGlyAlaHisLysAspCysGluValAlaProLeuProThrIleTyrLys 168
                                                                                                                                                                                                                                                                                                                                                                                                                                        HisGluAspGluLysIleAsnIleTyrCysLeuSerCysGluValProThrCysSerLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GlnGlu---SerSerArgProLeuHisAlaLysAlaGluGlnHisLeuMetCysGluGlu 128
                            GlnSerMetGluGluProGlnMetAlaLeuTyrLeuGlnGlnAlaLysGluLeuIleAsn
                                                            CTCATCCAGCAGTACCAGGAGCAGCTGGACAAGTCCACAAAGCTGGTGGAAACTGCCATC
                                                                                                                      AGTGAGTTGCTGCAGCGGATCACGCAGGAGCAGGAGAAAAAGCTTAGCTTCATCGAGGCC
                                                                                                                                                                                GTAAAGGAAGAGCTGAGCCAGAAGTTTGACACGTTGTATGCCATCCTGGATGAGAAGAAA
                                                                                                                                                                                                                                           CAGACCATCATCACTCAGCTGGAGGATTCCCCGTCGAGTGACCAAGGAGAACAGTCACCAG
                                                                                                                                                                                                                                                                 GlnAlaValIleThrGlnMetGluGluValCysGlnThrIleGluAspAsnSerArgArg
                                                                                                                                                                                                                                                                                                       GACAAAAGACTGAACTGAATAACTGTATCTCCATGCTGGTGGCGGGGAATGACCGTGTG
                                                                                                                                                                                                                                                                                                                                ArgGlnLysSerGluLeuSerAspGlyIleAlaMetLeuValAlaGlyAsnAspArgVal 188
                                                                                                                                                                                                                                                                                                                                                                                                                            CACGAAGATGAGAAAATCAACATCTACTGTCTCACGTGTGAGGTGCCCACCTGCTCCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAGGAGTGCTCCAGTCGGCCGCTG-----CAGAAGGGCAGTCACCCCATGTGCAAGGAG
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Matches:
Conservative:
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                                                                         including: arteriosclerosis, cirrhosis, hepatitis, cancers, AIDS, allergies, anaemia, asthma, autoimmune thyroiditis, bronchitis, atopic dermatitis, diabetes mellitus, emphysema Goodpasture's syndrome, gout, Grave's disease, multiple sclerosis, osteoarthritis, pancreatitis, psoriasis, rheumatoid arthritis, systemic lupus erythematosus, ulcerative colitis, uveitis, Alzheimer's disease, Huntington's disease, Parkinson's
                                                                                                                                                                                                                                                The present sequence is the coding sequence for a human transcription factor. The transcription factor and its coding sequence are useful in the diagnosis, treatment and prevention of diseases associated with altered expression of the transcription factor e.g. cell proliferative, autoimmune/inflammatory, neurological and developmental disorders. A number of specific disorders/diseases are given in the specification,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 11; Page 311; 327pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel transcription factor polypeptides, used to treat diseases associated with altered activity and expression of TRFX, and to for agents capable of modulating its activity - \frac{1}{2}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hillman JL,
Azimzai Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               autoimmune disease; inflammation; neurological disease;
developmental disorder; cancer; AIDS; infection; cytostatic; anti-HIV;
neuroprotective; antiinflammatory; gene therapy; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LysValGlyAlaMetSerLysValGluLeuAlaGlyArgProGluProGlyTyrGluSer
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                                                          stroke, and viral, bacterial,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard;
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P, Shah
                                                       protozoal
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P, Au-You
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Alignment Scores:

Sequence 1764

BP;

473 A;

399 C; 516 G;

376

T; 0 other;

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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                      GlyGluLeuLeuGlnAlaLeuAlaArgGluGlnGluCluLysLeuGlnArgValArgGly
                                                                                                                                                                                                                                                                                      CAGACCATCATCACTCAGCTGGAGGATTCCCCGTCGAGTGACCAAGGAGAACAGTCACCAG
                                                                                                                                                                                                                                                                                                             GlnAlaValIleThrGlnMetGluGluValCysGlnThrIleGluAspAsnSerArgArg
                                                                                                                                                                                                                                                                                                                                                                                                                             CACGAAGATGAGAAAATCAACATCTACTGTCTCACGTGTGAGGTGCCCACCTGCTCCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAGGAGTGCTCCAGTCGGCCGCTG-----CAGAAGGGCAGTCACCCCATGTGCAAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HisGlyValTyrGlyLeuGlnArgAsnLeuLeuValGluAsnIleIleAspIleTyrLys
                                                                                            {\tt GlnSerMetGluGluProGlnMetAlaLeuTyrLeuGlnGlnAlaLysGluLeuIleAsn}
                                                                                                                                           AGTGAGTTGCTGCAGCGGATCACGCAGGAGCAGGAGAAAAAGCTTAGCTTCATCGAGGCC
                                                                                                                                                                                                                                         GTAAAGGAAGAGCTGAGCCAGAAGTTTGACACGTTGTATGCCATCCTGGATGAGAAGAAA
                                                                                                                                                                                                                                                              GlnLysGlnLeuLeuAsnGlnArgPheGluThrLeuCysAlaValLeuGluGluArgLys
ATGGACTTCTTTACTTTGGATTTAGAGCACATAGCAGACGCCCTGAGAGCCCATTGACTTT

      MetGluGlnPheSerValSerValGluHisValAlaGluMetLeuArgThrIleAspPhe

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                                           ### AGCATTGTGGAAGCTTCCAAGGGCTGCCAGCTGGGGAAGAGCAGGGCTTTGAGAAC
                                                                    LysValGlyAlaMetSerLysValGluLeuAlaGlyArgProGluProGlyTyrGluSer
                                                                                                                                                                 LeuIleArgGlnTyrGlyAspHisLeuGluGlySerSerLysLeuValGluSerAlaIle
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1098.50
78.00%
60.00%
57.45%
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Matches:
Conservative:
Mismatches:
Indels:
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14-AUG-2000;
18-AUG-2000;
22-AUG-2000;
22-AUG-2000;
22-AUG-2000;
23-AUG-2000;
30-AUG-2000;
01-SEP-2000;
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14 - AUG - 2000;
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30-JUN-2000;
07-JUL-2000;
07-JUL-2000;
11-JUL-2000;
11-JUL-2000;
14-JUL-2000;
26-JUL-2000;
26-JUL-2000;
14-AUG-2000;
14-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vulnerary; secreted protein; rheumatoid arthritis; hyperproliferative disorder; cardiavascular disorder; cardiavascular disorder; cerebrovascular disorder; cerebral isordeemia; angiogenesis; nervous system disorder; cardiaver's disease; infection; ocular disorcerneal infection; wound healing; epithelial cell proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; opthalmalo vulnerary; secreted protein; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; immunosuppressive; antiarthritic; ss; antirheumatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human cDNA encoding a novel secreted protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1095
                                                                                                                                                                                         14-AUG-2000;
14-AUG-2000;
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2000US-0180628
2000US-0184647
2000US-01846350
2000US-0190874
2000US-0190875
2000US-0209467
2000US-0216487
2000US-0216487
2000US-0216880
2000US-0217487
2000US-0217487
2000US-0217487
2000US-0217487
2000US-0218290
2000US-02218290
2000US-0224518
2000US-0225267
2000US-0225267
2000US-0225267
2000US-0225275
2000US-0225758
2000US-0225758
2000US-0225758
2000US-0225758
2000US-0225758
2000US-0225758
2000US-0225758
2000US-0225758
                        2000US-0226868.
2000US-0227182.
2000US-0227009.
2000US-0228924.
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                                                                                                                                                                       Alignment Scores: Pred. No.:
                                                                                                                                                                                                                                             The invention relates to isolated nucleic acid molecules and their concoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or amelicrate a medical condition in e.g. humans, mice, crabbits, goats, horses, cats, dogs, chickens or sheep. They care also used in diagnosing a pathological condition or susceptibility to a pathological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in conditions or susceptibility continuous to be used in alleviating symptoms associated with the disorders and in conditions or susceptibility. Insorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, carebrovascular disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. neoplasms of the breast or liver, cardiovascular disord
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid molecules encoding 461 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions used as food additives or preservatives -  \frac{1}{2} \sum_{i=1}^{n} \frac{1}{
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29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000;

08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 20-OCT-2000; 20-OCT-2000; 01-NOV-2000;

08-NOV-2000; 08-NOV-2000;

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                           GlyGluGluGlyAsnAlaGlyLeuGluGlu 354
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19-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                    infection, or may result from an autoimmune disorder, a coagulation disorder (e.g. haemophilia), inhibition of tumour cell proliferation, suppression of an inflammatory response or treatment of a nervous system disorder such as Alzheimer's disease. Detection of the presence or increased expression of the polynucleotide or the protein it encodes is useful for the diagnosis and/or prognosis of one or more types of cancer. The polynucleotide and polypeptide can be used as nutritional sources or supplements and in the screening of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAH90117 standard; cDNA; 1183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            be genetic, may be caused by a viral (e.g. HIV), bacterial or fungal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                expressed in the bone marrow. The polynucleotide and the polypeptide encoded by it are useful in the treatment of various immune deficiencies and disorders. The deficiencies and disorders may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 608-609; 648pp; English.
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                                                                                                                                                                                                                                                                        Sequence 1183
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Zhou P,
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2000US-0662191.
2000US-0693036.
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P, Drmanac RT;
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987.50
81.97%
63.61%
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                                                                                                                                                                                                                       1009
Human; bone marrow; antiinflammatory; cytostatic; neuroprotective;
                                        Human bone marrow cDNA, SEQ ID NO: 55
                                                                                                                                                AAH89924 standard; cDNA; 1796
                                                                                                                                                                                                                                                                                             949
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                                                                                                                                                                                                                                                 LysValGlyAlaMet-----SerLysValGluLeu 298
                                                                                                                                                                                                                   TGGGTGGGGTCAGTTCAACTCTACAGCTCTAAGGTTCAAGTT 1050
                                                                                                                                                                                                                                                                                    CAGTCCCTGGACGAGCCTGGGGGAGCCACCTTCCTCTTGGTGAGCAGGACTAGAAGGGTC 1008
                                                                                                                                                                                                                                                                                                                      {\tt GlnSerMetGluGluProGlnMetAlaLeuTyrLeuGlnGlnAlaLysGluLeuIleAsn}
                                                                                                                                                                                                                                                                                                                                                         CTCATCCAGCAGTACCAGGAGCAGCTGGACAAGTCCACAAAGCTGGTGGAAACTGCCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                               GlyGluLeuLeuGlnAlaLeuAlaArgGluGlnGluGluLysLeuGlnArgValArgGly
                                                                                                                                                                                                                                                                                                                                                                                        \texttt{LeuIleArgGlnTyrGlyAspHisLeuGluGlySerSerLysLeuValGluSerAlaIle}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTAAAGGAAGAGCTGAGCCAGAAGTTTGACACGTTGTATGCCATCCTGGATGAGAAGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GlnLysGlnLeuLeuAsnGlnArgPheGluThrLeuCysAlaValLeuGluGluArgLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CysLysValPheGlyAlaHisLysAspCysGluValAlaProLeuProThrIleTyrLys 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CACGAAGATGAGAAAATCAACATCTACTGTCTCACGTGTGAGGTGCCCCACCTGCTCCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HisGluAspGluLysIleAsnIleTyrCysLeuSerCysGluValProThrCysSerLeu 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GlnGlu---SerSerArgProLeuHisAlaLysAlaGluGlnHisLeuMetCysGluGlu 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CACGGAGTGTACGGCCTGCAGAGGAACCTGCTGGTGGAGAACATCATCGACATCTACAAA 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HisGlyValTyrGlyLeuGlnArgAsnLeuLeuValGluAsnIleIleAspIleTyrLys 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ValSerSerGlyGlyArgPheArgCysProSerCysArgHisGluValValLeuAspArg 89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          {\tt CysAlaAsnAspValPheGlnAlaSerAsnProLeuTrpGlnSerArgGlySerThrThr}
                                                                          (first entry)
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                                                                                                                                                                   Query Match:
                                                                                                                                                                                Best Local
                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                          Alignment Scores:
                                                                                                                                                                                                                                                                                                         infection, or may result from an autoimmune disorder, a coagulation disorder (e.g. haemophilia), inhibition of tumour cell proliferation, suppression of an inflammatory response or treatment of a nervous system disorder such as Alzheimer's disease. Detection of the presence or increased expression of the polynucleotide or the protein it encodes is useful for the diagnosts and/or prognosts of one or more types of cancer. The polynucleotide and polypeptide can be used as nutritional sources or supplements and in the screening of chemical commons.
                                                                                                                                                                                                                                                                                                                                                                                                                                  expressed in the bone marrow. The polynucleotide and the polypeptide encoded by it are useful in the treatment of various immune deficiencies and disorders. The deficiencies and disorders may be genetic, may be caused by a viral (e.g. HIV), bacterial or fungal
                                                                                                                                                                                                                                                                         Sequence 1796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is one of 251 novel human polynucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 243-244; 648pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antiviral; antibacterial; antifungal; anti-HIV; haemostatic; immunosuppressive; gene therapy; cytokine cell proliferation; cell differentiation modulator; immune disorder; infection; cancer; cell differentiation modulator;
                                                                                                                                                                                                                             No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel bone-marrow-expressed polynucleotides and polypeptides, useful for treating e.g. cancer and immune deficiency disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ren
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HYSE-) HYSEQ INC
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25-APR-2000;
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                                                              172
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19-OCT-2000;
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                                                                         11 LeuGlyAspAlaHisAsnMetAspAsnLeuGluLysGlnLeuIleCysProIleCysLeu
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Rhr
              Glu-MetPheSerLysProValValIleLeuProCysGlnHisAsnLeuCysArgLysCy
GAGATTGTGTACCAAGCCCGTGGTCATCCTGCCGTGCCAGCACCAGCTGTGCCGGAAGTG
                                                        CTCCAGGATGGGAATCCCATGGAGAACTTGGAGATGCAGCTGATCTGGCCTATCTGCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001-488707/53.
                                                                                                                                                                                 Similarity:
                                                                                                                                                                                                                                                                                                    compounds as potential drugs.
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2000US-0553317.
2000US-0598042.
2000US-0598042.
2000US-0620312.
2000US-0653450.
2000US-0663191.
2000US-0693036.
2000US-0250583.
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Werhman T,
                                                                                                                                                  9.9e-81
920.50
69.23%
52.52%
48.14%
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u C, Xue AJ,
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Conservative:
Mismatches:
Indels:
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                                                                     AAC75285 standard; cDNA; 531 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCATCCAGCAGTACCAGGAGCAGCTGGACAAGTCCACAAAGCTGGTGGAAACTGCCATCC
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                                                                                                                                                                                                                                                                                  TGGACTTCTTTACTTTGGATTTAGAGCACATAGCAGACGCCCTGAGAGCCATTGACTTTG 1130
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(first entry)
                                                                                                                                                              -GlyGluGluGlyAsnAlaGlyLeu 352
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Human ORFX ORF840 polynucleotide sequence SEQ ID NO:1679

vulnerary; antiporiatic; antiparkinsonian; notropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiaflammatory; antiviral; antibacterial; antifungal; antirheumatic; antithyroid; antiviral; entibacterial; antifungal; antirheumatic; antithyroid; antiviral; antibacterial; antibacter; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation; thomboglob; cartilage damage; antiinflammatory disease; coagulation; thrombosis; contraceptive; ss. Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; nootropic; neuroprotective;

WO200058473-A2

05-OCT-2000

31-MAR-2000; 2000WO-US08621.

밁 δÃ В 20 8 Дb δÃ Db δÃ В

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31-MAR-1999; 02-APR-1999; 05-APR-1999; 30-MAR-2000; 2000US-0540763 99US-0127607. 99US-0127636. 99US-0127728.

(CURA-) CURAGEN CORP.

Shimkets RA, Leach M;

2000-602362/57.

AAB41076.

Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -

Claim 5; Page 1334; 5507pp; English.

antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; antiparkinsonian; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antibacterial; antivital; antifungal; antirheumatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive. nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, dilabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary;

γ 밁 δõ 밁 Qy 밁 δÃ Db Qy 밁 Š В Š рЬ ρ

Sequence 531 BP; 129 A; 143 C; 150 G; 108 T; 1 other;

Percent Similarity:
Best Local Similarity: Score: No.: 9.1e-56 659.50 88.16% 78.95% Matches: Conservative: Mismatches:

Leach MD,

Shimkets

2002-106200/14.

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hypothyroidism; cholesterol ester storage disease; infection; vulnerary; vasotropic; antipsoriatic; antidiabetic; cytostatic; nootropic; neuroprotective; antieherosclerotic; anticoagulant; thrombolytic; cardiant; hypotensive; antithyroid; antiinflammatory; immunomodulator;
                                                                                                                                                                                                                                                                                                                                Human; ORF; open reading frame; ORFX; drug screening; diagnosis; disease monitoring; cytokine; cell proliferation; cell differentiation; immune modulation; haematopoiesis regulation; tissue growth; angiogenesis; activin; inhibin; chemotactic; chemokinetic; haemostatic; thrombolytic; tumour inhibition; bodily characteristic; fertility; behaviour; cancer; proliferative disorder; neurological disorder;
                                                                                                                                                  WO200190366-A2
                                                                                                                                                                                                                  dermatological; analgesic; virucide; antibacterial; fungicide; gene; ss
                                                                                                                                                                                                                                                                                                 cardiovascular disease; immune system disorder; organ transplantation; tissue growth disorder; tissue regeneration disorder; diabetes mellitus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human interleukin receptor-like ORF3051 cDNA, SEQ ID NO:6101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABN78104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABN78104 standard; cDNA;
             (CURA-) CURAGEN CORP
                                                24-MAY-2000; 2000US-206690P
                                                                                24-MAY-2001; 2001WO-US17076
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LeuGluMetPheSerLysProValValIleLeuProCysGlnHisAsnLeuCysArgLys 49
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ValSerSerGlyGlyArgPheArgCysProSerCysArgHisGluValValLeuAspArg

TGTGCCAATGACATCTTCCAGGCTGCAAATCCCTACTGGACCAGCCGGGGCAGCTCAGTG CysAlaAsnAspValPheGlnAlaSerAsnProLeuTrpGlnSerArgGlySerThrThr CTGGAGATGTTTACCAAGCCAGTGGTCATCTTGCCGTGCCAGCACAACCTGTGCCGGAAG

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69 20:

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US-09-908-988B-2 (1-366) x ABN78104 (1-531)

10 LeuLeuGlyAspAlaHisAsnMetAspAsnLeuGluLysGlnLeuIleCysProTleCys

CTGATCCAGGATGGGAATCCCATGGAGAACTTGGAGAAGCAGCTGATCTGCCCTATCTGC

LeuGluMetPheSerLysProValValIleLeuProCysGlnHisAsnLeuCysArgLys

49

Query Best Local Percent Similarity:

Similarity:

9.1e-56 659.50 88.16% 78.95% 34.49%

Indels: Mismatches: Conservative: Matches:

531 120 14 15 3

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CC cell differentiation, immune modulation, hamatopolesis regulation, continuous, continuo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                designated ORF (Open reading frame) 1.4534, and sequences ABN75054-
ABN79587 represent cDNAs encoding them. The invention also encompasses
polypeptides at least 80% identical to the ORF1-ORF4534 (collectively
referred to as ORFX) proteins, polynuclectides at least 85% identical to
the ORFX nucleic acid sequences, vectors and host cells comprising ORFX
polynucleotides, the recombinant production of ORFX proteins, antibodies
specific for ORFX proteins, methods of detecting ORFX polynucleotides and
polypeptides, methods of screening for modulators of ORFX expression or
activity, and methods of screening individuals for a predisposition to an
ORFX-associated disorder. The ORFX proteins of the invention have a wide
range of biological activities, such as cytokine, cell proliferation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 1775; 2508pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and disorders related to organ
Sequence 531
                                                                 diagnosis, treatment and monitoring of ORFX-associated diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequences ABP31028-ABP35561 represent 4534 novel human proteins
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129 A; 143
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   G; 108
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RESULT 18
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07-JUL-2000;
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17-MAR-2000;
18-APR-2000;
19-MAY-2000;
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24-FEB-2000;
02-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; immunosuppressive; antiarthritic; ss; antirheumatic; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; opthalmalogical; vulnerary; secreted protein; rheumatoid arthritis; hyperproliferative disorder; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; cerebral ischaemia; anglogenesis; nervous system disorder; cardimer's disease; infection; ocular disorder; corneal infection; wound healing; epithelial cell proliferation; skin ageing; food additive; preservative; antiproliferative.
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CC encoded secreted proteins. The nucleic acids and proteins are used to CC prevent, treat or ameliorate a medical condition in e.g. humans, mice, CC rabbits, goats, horses, cats, dogs, chickens or sheep. They CC are also used in diagnosing a pathological condition or susceptibility CC to a pathological condition. Antibodies to the proteins can also CC be used in alleviating symptoms associated with the disorders and in CC diagnostic immunoassays e.g. radioimmunoassays or enzyme linked CC immunosorbant assays (ELISA). Disorders which are diagnosed or treated CC include autoimmune diseases e.g. rheumatoid arthritis, CC hyperproliferative disorders e.g. neoplasms of the breast or liver, CC cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders CC e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. CC Alzheimer's disease, infections caused by bacteria, viruses and funging collar disorders e.g. corneal infection, and many other CC disorders listed in the specification. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to CC prevent skin aging due to sunburn, to maintain organs before CC transplantation, for supporting cell culture of primary tissues, to CC as a food additive or preservative to increase or decrease storage CC canabilities, fat content, lipid, protein, case or decrease storage CC canabilities, fat content, lipid, protein, case or decrease storage
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                   capabilities,
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MILLENNIUM PREDICTIVE MEDICINE INC
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; 2000US-189862P.
; 2000US-207454P.
; 2000US-211314P.
; 2000US-219007P.
; 2000US-255281P.
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                                                                                                                                                                                         expression marker cDNA 21910.
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marker; gene; ss.
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(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             selecting a composition for inhibiting prostate cancer in a patient; assessing the prostate cell carcinogenic potential of a compound; determining whether prostate cancer has metastasized in a patient; assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                                                                                           Gly-----SerThrThrValSerSerGlyGlyArgPheArgCysProSerCysArg
                                                                                                                                                                                                                                                                                                                                                      AsnLeuGluLysGlnLeuIleCysProIleCysLeuGluMetPheSerLysProValVal 38
                         TGTAAACCACCACCTCAAGAATCCACAAAAAGCTGCATGGACTGTAGTGCAAGTTACTGC
                                                                                                          AsnIleIleAspIleTyrLys-------
                                                                                                                                     CATGATGTGGATCTTGGAGAACGAGGAATCAATGGTCTGTTTCGAAACTTCACTTTGGAA
                                                                                                                                                            HisGluValValLeuAspArgHisGlyValTyrGlyLeuGlnArgAsnLeuLeuValGlu
                                                                                                                                                                                                                                                CTCCCCTCCCTAGTATGGATAAAATTGACCGAATTAACAGACCAGGCTGGAAGCGCAAT
                                                                                                                                                                                                                                                                                                    GATGATTCATCAACGATGTGGGATCAGACAACTCCAATCAAAGCAGTCCTCGACTTCGG
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                                                                                ACTATTGTGGAAAGATATCGTCAAGCAGCTAGGGCAGCCACAGCCATTATGTGTGACCTT
                                                                                                                                                                                              TCATTGACCCCGAGGACAACTGTT---
                                                                                                                                                                                                                                                                                                                                                                                    IleLeuProCysGlnHisAsnLeuCysArgLysCysAla------
                                                                                                                                                                                                                                                                                                                                 ------AsnAspVal------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1321 A;
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427.50
44.30%
28.35%
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23
                                                      -GlnGluSerSerArg
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ProLeuHisAlaLysAlaGluGlnHis--
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Mismatches:
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RESULT 20
ABV22250/G
ID ABV222
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XX Human
DE Human
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09-JUN-2000;
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                                                                                                                                                                                                                                                                     prostate
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2000US-183319P.
2000US-189862P.
2000US-207454P.
2000US-211314P.
2000US-2119107P.
2000US-255281P.
                                                                                                                    2001WO-US05171
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                                                                                                                                                                                                                                                      gene;
                                                                                                                                                                                                                                                                     cytostatic;

    LeuMetCysGluGluHisGluAspGluLys 133

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DB:
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Best Local Similarity:
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Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
(e) selecting a composition for inhibiting prostate cancer in a patient;
(f) assessing the prostate cell carcinogenic potential of a compound;
(g) determining whether prostate cancer has metastasized in a patient;
(h) assessing the aggressiveness or indolence of procession.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer -
                                                                                                                                                                                                               3645 TCATTGACCCCGAGGACAACTGTT------
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                                                                                                      AsnIleIleAspIleTyrLys----
                                                                                                                                                            HisGluValValLeuAspArgHisGlyValTyrGlyLeuGlnArgAsnLeuLeuValGlu 102
TGTAAACCACCACCTCAAGAATCCACAAAAAGCTGCATGGACTGTAGTGCAAGTTACTGC 3421
                                                                      ACTATTGTGGAAAGATATCGTCAAGCAGCTAGGGCAGCCACAGCCATTATGTGTGACCTT
                                                                                                                                          CATGATGTGGATCTTGGAGAACGAGGAATCAATGGTCTGTTTCGAAACTTCACTTTGGAA
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                                     -GlnGluSerSerArg-----
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                                                                                                                                                                                                                                                                                                                --PheGlnAlaSerAsnProLeuTrpGlnSerArg
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Search completed: December 3, 2002, 14:10:55 Job time: 299 secs

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OM protein - nucleic search, using frame_plus_p2n model
  December
                                                                                                                              Copyright
3, 2002, 14:05:55; Search time 2707 Seconds
                                                                                                                            GenCore version 5.1.3 (c) 1993 - 2002 Compugen Ltd
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Title: Perfect score: on: US-09-908-988B-2 1912 (without alignments)
3934.846 Million cell updates/sec

Scoring table: MNFTVGFKPLLGDAHNMDNL....EGNAGLEEERLDVPEGSGLH 366

BLOSUM62

Searched: Xgapop 10.0, Ygapop 10.0, Fgapop 6.0, Delop 6.0, 2054640 seqs, 14551402878 residues Xgapext Ygapext Fgapext Delext 0.5 7.0 7.0

Minimum DB seq length: 0
Maximum DB seq length: 200000000 Total number of hits satisfying chosen parameters:

4109280

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Command line parameters:

WWDEL-framet_p2n.model -DEV-xlh
-Q-/Cgn2_1/USPTO_spool/US09908988/runat_26112002_112154_11224/app_query.fasta_1
-Q-/Cgn2_1/USPTO_spool/US09908988/runat_26112002_112154_11224/app_query.fasta_1
-DB-GenEmbl -QFMT-fastap -SUFFIX=rge -MINMATCH-0.1 -LOOPCL-0 -LOOPEXT=0
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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                                                                            Spencer, J.A., Eliazer, S., Ilaria, R.L. Jr., Richa Olson, E.W.
Regulation of microtubule dynamics and myogenic MURF, a striated muscle RING-finger protein J. Cell Biol. 150 (4), 771-784 (2000) 20411220
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Submitted (09-AUG-2000) Molecular
Blvd., Dallas, TX 75390-9148, USA
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Spencer, J.A. and Olson, E.N.
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ThrileGluAspAsnSerArgArgGlnLysGlnLeuLeuAsnGlnArgPheGluThrLeu 220
                                                                                                                                                                                                                         CysGluValProThrCysSerLeuCysLysValPheGlyAlaHisLysAspCysGluVal 160
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                                                                                     LeuValAlaGlyAsnAspArgValGlnAlaValIleThrGlnMetGluGluValCysGln
                                                                                                                                     GCCCCTCTGCCCACCATTTACAAACGCCAGAAGAGTGAGCTGAGCGATGGCATCGCGATG
                                                                                                                                                       AlaProLeuProThrIleTyrLysArgGlnLysSerGluLeuSerAspGlyIleAlaMet
                                                                                                                                                                                                       TGCGAGGTGCCCACCTGCTCTCTGCAAGGTTTTCGGCGCCCACAAGGACTGTGAGGTG
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PILCAVLEERKGELLQALAREQEEKLQRVGALTTOMEEVCQTIEDMSRROKQOLLNQRFE
TLCAVLEERKGELLQALAREQEEKLQRVGRLTRQYGDHLEGSSKLVESAIQSMEEPQM
ALYIQQAKELINKVGAMSKVELAGRPEPGYESMEQFSVSVEHVAEMLRTIDFQPGAAG
DEEDDDMALDGEEGNAGLEERKLDVPEGSGLH"
384 c 473 g 236 t
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199. .1299
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                                                                                                                                                                                                                     Direct Submission
Submitted (12-FEB-2001) Centner T.,
Meverhofstrasse 1,
                                                                                                                                                                                                                                                                                                                                                              Centner,T., Yano,J., Kimura,E., McElhinny,A.S., Pelin,K., Witt,C.C., Bang,M.L., Trombitas,K., Granzier,H., Gregoric Sorimachi,H. and Labeit,S.
                                                                                                                                                                                                          EMBL-Heidelberg, Meyerhofstrasse Revised by author 22-FEB-2001
                                                                                                                                                                                                                                                                                                                  Identification of muscle specific ring regulators of the titin kinase domain J. Mol. Biol. 306 (4), 717-726 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                    EUKATYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 1329)
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                                                                     /gene="RNF30"
49. .1203
                                                                                                /evidence=not_experimental
49. .1203
/product="ring finger
/protein_id="CAC32842.
                           /codon_start=1
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                                                                                                                          /note="putative alternative
                                                                                                                                                                 /organism="Homo sapiens"
                                                                                                                                                     /db_xref="taxon:9606"
                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                       translation initiation codon"
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                                    GCCCCACTGCCCACCATTTACAAACGCCAGAAGAAACAGGATCTCACTCTGTTGCCCAGG
                                                        AlaProLeuProThrIleTyrLysArgGlnLys-----
                                                                                                                                 CysGluValProThrCysSerLeuCysLysValPheGlyAlaHisLysAspCysGluVal 160
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/protein_id="cAc32841.1"
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KAEQHLMCEEHEEEKINIYCLSCEVPTCSLCKVFGAHKDCEVAPLPTIYERQKNELSD
GIAMLVAGNDRVQAVITQMEEVCQTIEDNSRRQKQLLTQRFESLCAVLERKGELLQA
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MSKVELAGRPEPGYESMEQFTVRVEHVAEMLRTIDFQPGASGEEEEVAPDGEEGSAGP
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RQYGGHLEASSKLVESAIQSKEEPQMALYLQQAKELINKVGAMSKVELAGREEPGYES
MEQETVRVEHEVAEMLKTIDFOÇGASGEEEEVAPDGEEGSAGPEEERPDGP"
join(49...515,642...1203)
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/note="short isoform"
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1 (bases 1 to 1500)

Lal, P., Yue, H., Tang, Y.T., Baughn, M.R., Azimzai, Y. and Tran, B. Human transcriptional regulator proteins

Patent: WO 0078954-A 54 28-DEC-2000;

Incyte Genomics, Inc. (US)
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YGILEERKTEMTQAITRTQEEKLEHYRTLIRKYSDHLENVSKLYESGIQFMDEFEMAV
FLQNAKTLLQKIYEASKAFQMEKLEQGYEIMSNFTVNLNREEKIIREIDFSREEEEEEE
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/db_xref="G1:21533715"
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NIIDIYKQESTRPEKKLDQPMCEEHEEERINIYCLNCEVPTCSLCKVFGAHKDCQVAP
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                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                       Submitted (11-MAY-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                        NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Library Preparation: Rul
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Rubin Laboratory
The I.M.A.G.E. Consortium (LLNL)
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81 CysArgHisGluValValLeuAspArgHisGlyValTyrGlyLeuGlnArgAsnLeuLeu 100
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                                                                                                                        TATTTGCCCACAAGAGGAGGTACCACCATGGCATCAGGGGGCCGATTCCGCTGCCCATCC
                                                                                                                                                                                                                                                                                                                                              ProCysGlnHisAsnLeuCysArgLysCysAlaAsnAspValPheGlnAlaSerAsnPro
                                                                                                                                                                         LeuTrpGlnSerArgGlySerThrThrValSerSerGlyGlyArgPheArgCysProSer
                                                                                                                                                                                                                                                                                                      CCTTGTCAGCACAACCTGTGTAGGAAATGTGCCAGTGATATTTTCCAGGCCTCTAACCCG
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This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: nisc_mgc@nhgri.nih.góv
Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Benjamin,B., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.,
Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCLoskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zhang, L.-H. and Green, E.D.
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/translation="MDNLEKQLICPICLEMFTKPVVILPCOHNLDYKQESTRPEKK
/translation="MDNLEKQLICPICR"
/translation="MDNLEKQ
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GEAVEVEEVENVQTEFPGEDENPEKASELSQVELQAAPGALPVSSPEPPPALPPAADA
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/tissue_type="Muscle, rhabdomyoss
/clone_lib="NIH_MGC_17"
/lab_host="DH10B-R"
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                                                                                                         oligo capping; fis (full insert sequence).
Homo sapiens heart cDNA to mRNA, clone_lib:HEART2
Nishi,T., Ota
Sugiyama,T.,
                                                                            Homo sapiens
                                                                                            clone: HEART2001931.
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                                               Mammalia;
                   Ota,T.,
                                               Eutheria;
                                                              Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
   Irie, R., Otsuki, T.,
                 Nakagawa, S., Senoh, A., Mizuguchi, H., Inagaki, H.,
                                               Primates;
                                              Catarrhini; Hominidae;
   Sato, H.,
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   Wakamatsu,A.,
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   Ishii, S.,
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TGCGAAGTACCCACCTGCTCTCTGTGCAAGGTGTTTGGTGCACACAAAGACTGCCAGGTG
                                                                                           GluGlnHisLeuMetCysGluGluHisGluAspGluLysIleAsnIleTyrCysLeuSer 140
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                                                                       TCCGACCAGCCCATGTGCGAGGAACATGAAGAGGAGCGCATCAACATCTACTGTCTGAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hrl.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center wational Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and Evaluation; clone selection for full insert sequencing: HRI and RAB.
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Isogai,T. and Yamamo
Direct Submission
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/clone_lib="HEART2"
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                          Submitted (12-FEB-2001) Centner T., Structure and Biocomputing, EMBL-Heidelberg, Meyerhofstrasse 1, Heidelberg 69112, Germany Revised by author 22-FEB-2001
                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2202)
Centner, T., Yano, J., Kimura, E., McElhinny, A.S., Pelin, K., Witt, C.C., Bang, M.L., Trombitas, K., Granzier, H., Gregorio, C.C., Sorimachi, H., and Labeit, S.
                                                                                               Centner, T
                                                                                                                                                     Identification of muscle specific ring finger proteins as regulators of the titin kinase domain J. Mol. Biol. 306 (4), 717-726 (2001)
                                                                             Direct Submission
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finger protein 29; RNF29 gene
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                                                                 CysArgHisGluValValLeuAspArgHisGlyValTyrGlyLeuGlnArgAsnLeuLeu
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KAFQMEKIEHGYENNNHFTYNLNREEKIIRELDFYREDEDEEEEEGGEGEKEGEGEGEVG
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PVTQ1GFEAPPLQGQAAAPASGSGADSEPARHIFSFSWLNSLNE"
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SDQPMCEEHEEERINIYCLNCEWPTCSLCKVFGAHKDCQVAPLTHYVGROKSELSDGI
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PVTQGEVYPTGSEQTTESETFVFAAAETADPLFYFSWYKGQTRKATTNPPCTPGSEGL
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/db_xref="taxon:9606"
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/protein_id="CAC32840.1"
/db_xref="GI:13160386"
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                                                                                                             oligo capping; fis (full insert sequence).
Homo sapiens normal dermal fibroblasts (Neonatal Skin) (NHDF2564)
CDNA to mRNA, clone_lib:DFNES2 clone:DFNES2007332.
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2634 bp mRNA linear PR
Homo sapiens cDNA FLJ33991 fis, clone DFNES2007332, mo
similar to Mus musculus RING-finger protein MURF mRNA.
Tashiro,H., Yamazaki,M., Watanabe,K., Kumagai,A., Itakura,S., Fukuzumi,Y., Fujimori,Y., Komiyama,M., Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakanatsu,A., Ishi,S., Yamamoto,J., Isono Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H.,
                                                                                                  Homo sapiens
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                                                                       ; Metazoa;
Eutheria;
                                                                       Chordata;
Primates;
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Catarrhini; Hominidae
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                          CysGluValProThrCysSerLeuCysLysValPheGlyAlaHisLysAspCysGluVal
                                                                                                   GluGlnHisLeuMetCysGluGluHisGluAspGluLysIleAsnIleTyrCysLeuSer
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Similarity:
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Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
NEDO human cDNA sequencing project
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                                                                                                                                 A novel RING finger protein associated with titin Unpublished
                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                       Homo sapiens titin zinc-finger anchoring protein, 50kDa isofaJ243488
AJ243488.1 GI:14588845
AJ243488.1 GI:14588645
alternative splicing; signal transduction; titin zinc-finger
                                                                                                                                                        Kelly, R., Neubauer, G. and Gautel, M.
                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                               anchoring protein;
                                                                                                                                                                      (bases 1 to 1810)
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_type="cardiomyocyte"
                                                                                                                                                                                                                                tizian
                                                                                                                                                                                                                                                                                                                                                                358
                                                                                                                                                                                                                                                                                        1810 bp
                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                      -GAAGGAGAAGTGGGAGGAGAAGCA 1435
                                                                                                                                                                                                                                                                                          mRNA
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Best Local Similarity: Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                        CysGluValProThrCysSerLeuCysLysValPheGlyAlaHisLysAspCysGluVal
                                                                                                                                                                                                                                                                                                                                                        GluLysGlnLeuIleCysProIleCysLeuGluMetPheSerLysProValValIleLeu
             ThrIleGluAspAsnSerArgArgGlnLysGlnLeuLeuAsnGlnArgPheGluThrLeu
                                                                                                                                                 AlaProLeuProThrIleTyrLysArgGlnLysSerGluLeuSerAspGlyIleAlaMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ProCysGlnHisAsnLeuCysArgLysCysAlaAsnAspValPheGlnAlaSerAsnPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATGAGCGCATCTCTGAATTACAAATCTTTTTCCAAAGAGCAGCAGACCATGGATAACTTA
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                                                     TGCGAAGTACCCACCTGCTCTCTGTGCAAGGTGTTTGGTGCACACAAAGACTGCCAGGTG
                                                                                                                                                                                                                                                                                 TCCGACCAGCCCATGTGCGAGGAACATGAAGAGGAGCGCATCAACATCTACTGTCTGAAC
                                                                                                                                                                                                                                                                                                     GluGlnHisLeuMetCysGluGluHisGluAspGluLysIleAsnIleTyrCysLeuSer
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                                                                                                                               GCTCCCCTCACTCATGTGTCCAGAGACAGAAGTCTGAGCTCAGTGATGGCATCGCCATC
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/protein_id="CAC43019.1"
/protein_id="CAC43019.1"
/db_xref="Gi:14588846"
/translation="MSASLNYKSFSKEQQTMDNLEKQLICPICLEMFTKPVVILPCQH
/translation="MSASLNYKSFSKEQQTMDNLEKQLICPICLEMFTKPVVILPCQH
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NIIDIYKOESTRPBKKSDQPMCEHBEBERINTYCLLCEVPTCSLCXVFGAHKDCQVAP
LTHVFQRQKSELSDGIAILVGSNDRVOGVISQLEDTCKTIEECCRKQKQELCEKFDYL
TGILEERKNEMTQVITRTQEEKLEHVFALIKKYSDHLENVSKLVESGIQFMDEPEMAV
ELQNAKTLIKKISBASKAFQMEKIEHYENNHETYNLMREEKIIREIDTYREDEDDE
EEEEGGEGEKEEEGEVGGEAVEVEEVENVQTEFFGEDENPEKASELSQVELQAAPGALP
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227. .1585
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/note="50kDa isoform
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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gautel, M.S.
Direct Submission
Submitted (29-JUN-1999) Gautel M.S., Physikalische Biochemie,
Max-Planck-Institut fuer molekulare Physiologie, Otto-Hahn-Strasse
11, Dortmund, 44227, GERMANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2098)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alternative splicing; signal transduction; titin zinc-finger anchoring protein; tizian.
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AJ243489.1 GI:14588847
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
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A novel RING finger protein associated with titin kinase
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                                                         /evidence=experimental
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227...1873
                                  FLQNAKTLLKKI SEASKAFQMEKI EHGYENMNHFTVNLNREEKI I REIDFYREDEDEE
                                                                                                                                                                                                                                                                                                                                                                                                                                    /function="putative role in signal transduction"
/note="60kDa isoform"
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EEEGGEGEKEEEGEVGGEAVEVEEVENVQTEFPGEDENPEKASELSQVELQAAPGALP
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ORIGIN
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VSSPEPPPALPPAADAPVTQGEVVPTGSEQTTESETPVPAAAETADPLFYPSWYKGQT
RKATTNPPCTPGSEGLGQIGPPGSEDSNYRKAEVAAAASERAAVSGKETSAPAATSQ
IGFEAPPLQGQAAAPASGSGADSEPARHIFSFSWLNSLNE"
632 a 497 c 534 g 435 t
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Scores: 1157.00 Matches: 2098 1157.00 Matches: 222 Anthes: 223 Similarity: 61.848 Conservative: 74 60.518 Mismatches: 10 Gaps: 74 61.848 Mismatches: 10 Gaps: 74 Findels: 10 Gaps: 10 MetAsnPheThrValGlyPheLysproLeuLeuGlyAspAlaHisAsnMetAspAll::: 11 ATGAGGCARCTCTGTGAATTACAAATCTTTTTCCAAAGAGAGAGAGAGA
Length: 2098 Similarity: 76.60%
는 불구분 첫 분 요구성 오구분 불··분 불구형 첫구성 불구형 오구병 첫구의 불구분 첫-S

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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                         Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathiewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smallus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
                                                                                                                                                                                                                                                                                                                    through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 15 Row: o Column: 19
This clone was selected for full length sequencing because it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tissue Procurement: ATCC/DCTD/DTP cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Genome Sequence Centre,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (09-OCT-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                    passed the following selection criteria:
    Location/Qualifiers
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BC015717.1
                                                                                                                                                                                                                                                                                                                                                                           Clone distribution: MGC clone distribution information can be found
                                                                                                                                                                                                                                                                                                                                                                                                                 George Yang, Scott Zuyderduyn, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BC Cancer Agency, Vancouver, BC, Canada
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Mammalia; Eutheria;
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IMAGE: 3922363,
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/clone_lib="NIH_MGC_72"
                                                                                                                                                                                                                            /organism="Homo sapiens"
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                                                                                                 /codon_start=1
                                                                                                                  /note="Vector: 135. .1175
                                                                                                                                                      /Lab_host="DH10B"
                                                                                                                                                                                                         /clone="MGC:17320 IMAGE:3922363"
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Percent Similarity:
Best Local Similarity:
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                                       CTCATCCAGCAGTACCAGGAGCAGCTGGACAAGTCCACAAAGCTGGTGGAAACTGCCATC
                                                                                                                   AGTGAGTTGCTGCAGCGGATCACGCAGGAGCAGGAGGAAAAGCTTAGCTTCATCGAGGCC
                                                                                                                                     GTAAAGGAAGAGCTGAGCCAGAAGTTTGACACGTTGTATGCCATCCTGGATGAGAAGAAA
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                                                                                                                                                                                                                                                                         CAGACCATCATCACTCAGCTGGAGGATTCCCCGTCGAGTGACCAAGGAGAACAGTCACCAG
                                                                                                                                                                                                                                                                                                             {\tt GlnAlaValIleThrGlnMetGluGluValCysGlnThrIleGluAspAsnSerArgArg}
                                                                                                                                                                                                                                                                                                                                                     GGACAAAAGACTGAACTGAATAACTGTATCTCCATGCTGGTGGCGGGGAATGACCGTGTG
                                                                                                                                                                                                                                                                                                                                                                         ArgGlnLysSerGluLeuSerAspGlyIleAlaMetLeuValAlaGlyAsnAspArgVal 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CysLysValPheGlyAlaHisLysAspCysGluValAlaProLeuProThrIleTyrLys
GlnSerMetGluGluProGlnMetAlaLeuTyrLeuGlnGlnAlaLysGluLeuIleAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CACGAAGATGAGAAAATCAACATCTACTGTCTCACGTGTGAGGTGCCCACCTGCTCCATG
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                                                                           LeuIleArgGlnTyrGlyAspHisLeuGluGlySerSerLysLeuValGluSerAlaIle
                                                                                                                                                                                                                                                                                                                                                                                                                                 TGCAAGGTGTTTGGGATCCACAAGGCCTGCGAGGTGGCCCCATTGCAGAGTGTCTTCCAG
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SVFQGQKTELNNCISMLVAGNDRVQTIITQLEDSRRVTKENSHQVKEELSQKFDTLYA
ILDEKKSELLQRITQEQEEKLSFIEALIQQYQEQLDKSTKLVETAIQSLDEPGGATFL
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63.36%
58.55%
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Matches:
Conservative:
Mismatches:
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927

CAGTCCCTGGACGAGCCTGGGGGGAGCCACCTTCCTTGACTGCCAAGCAACTCATCAAA

TITLE Identific		Qy 57 AlaSerAsnProLeuTrpGlnSerArgGlySerThrThrValSerSerGlyGlyArgPhe 76
Bod Cla Pan		Qy 37 ValValIleLeuProCysGlnHisAsnLeuCysArgLysCysAlaAsnAspValPheGln 56
Eukary Mammal Rattus	R	Oy 17 MetAspAsnLeuGluLysGlnLeuIleCysProIleCysLeuGluMetPheSerLysPro 36
3	SKE	Qy 4 ThrValGlyPheLys
DEFINITION RATTUS no: ACCESSION AY059627	DE AC	US-09-908-988B-2 (1-366) x AX418852 (1-1597)
T 14 627	AY AY	Indels: Gaps:
	Qy dd	4.06e-81 1110.00 78.53%
296 ValGluLeuAla	Ор	BASE COUNT 405 a 404 c 438 g 350 t ORIGIN
1112 GGGGCTACCTTO	ALC DP	THERNOSCHLYKTI VEVERINGE TERHTLY KRYLEROSINTVETALT KOJUDERGGATE SOAKQLI KSI VEASKGCQLGKT EQGFENMDY FTLDLEHI A EALRAI DFGTGKGCDVTC LTPERORSS"
276 MetAlaLeuTyı	PLQ LYA QY	DIYKQECSSRPLQKCSHPDKKINIYCLTCEVPTCSLCKVFGAHQACEVAPLQ SIPQQQKTELSNCISHVAGNDRVQTIISQLLDSCRVTKENSHQVKEELSQKFDTLYA TIPEVCKTI COLTRODECTVI CELTATI I CALEBOL PAGMATATOT DEBOCATION
		/translation="MDYKSSLIPDGNAMENLEKQLICPICLEMFTKPVVILPCQHNLC RKCANDIFQAANPYWTNRGGSVSMSGGRFRCPSCRHEVIMDRHGVYGLQRNLLVENII
	OV 50	/protein_de="CAD35457.1" /protein_id="CAD35457.1" /db_xref="GI:21523717"
:::	D	/node="monamed protein product" /noden start=1
932 AAGTTTGACACC	0	/organism="Mus musculis" /db_xref="taxon:10000"
	Qy	Location/Qualifiers 11597
872 GAGGACTCGTGC	מם	JOURNAL PATEMEDIACE FILAMETICS IN SCIENCE CELLS JOURNAL PATEMENTS THE UNIVERSITY OF TEXAS SYSTEM (US)
196 GluGluValCys	Qγ	AUTHORS Olson, E.N. and Spencer, J.A. TITLE Methods and compositions for stabilizing microtubules and
176 AspGlyIleAla ::: ::: 812 AACTGCATCTCC	S. Qy	
752 CAGGCCTGTGAG	Ф	NEIWOKUS . SOURCE house mouse. ORGANISM Mus musculus
156 LysAspCysGlu	Qy	AX418852 AX418852.1 GI:2152371
136 IleTyrCysLeu 692 ATCTACTGTCTC	02 Db	z
116 LeuHisAlaLys ::: 638 CTGCAG	Qy Db	
578 AGGAACCTGCTG	מם	Ov 329 GlnProGlvAlaAlaGlvAsnGlnGlnAsnAsnAsnAsnAsnAsnAsnAsnAsnAsnAsnAsnAsn
97 ArgAsnLeuLeu	Оу	309 MetGluGlnPheSerValSerValGluHisValAlaGluMetLeuArgThrIleAspPhe
77 ArgCysProSer	Qy Qy	987
	da d	Qy 289 LysvalGlyAlaMetSerLysValGluLeuAlaGlyArgProGluProGlyTyrGluSer 308

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S.C., Latres, E., Baumhueter, S., Lai, V.K.-M., Nunez, L., J.A., Poueymirou, W.T., Panaro, F.J., Na, E., Dharmarajan, K., Valenzuela, D.M., DeChiara, T.M., Stitt, T.N., 11.0s, G.D. and Glass, D.J. 11.0s, G.D. and Glass, D.J.
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.a; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
norvegicus
no
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                                          GluLysGlnLeuIleCysProIleCysLeuGluMetPheSerLysProValValIleLeu
                                                                                                                       AlaGluGlnHisLeuMetCysGluGluHisGluAspGluLysIleAsnIleTyrCysLeu 139
                                                                                                                                                                                 ValGluAsnIleIleAspIleTyrLysGlnGlu---SerSerArgProLeuHisAlaLys
                                                                                                                                                                                                                                                                                        TACTGGACCAACCGCGGTGGCTCGGTGTCCATGTCTGGAGGTCGTTTCCGCTGCCCCTCG
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/strain="Sprague-Dawley"
/db_xref="taxon:10116"
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RKCANDIFQAANPYWTNRGGSVSMSGGRFRCPSCRHEVIMDRHGVYGLQRNLLVENII
DIYKOECSSRPLOKGSHPWCKEHEDEKINIYCLTCEVPTCSLCKVFGAHQACEVAPLQ
SIFQGQKTELSNCISMLVAGNDRVQTIISQLEDSCRVTKENSHQVKEELSHKPDALYA
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LSAKPLIKSIVEASKGCQLGKTEQGFENMDYFTLNLEHIAEALRAIDFGTDEEEEFFTE
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/protein_id="AAL16405.1"
/db_xref="GI:16444656"
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                                                                                              Submitted (12-FEB-2001) Centner T., EMBL-Heidelberg, Meyerhofstrasse 1, Revised by author 22-FEB-2001
                                                                                                                                                                                                                                                          Identification of muscle specific ring regulators of the titin kinase domain J. Mol. Biol. 306 (4), 717-726 (2001)
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Centner,T., Yano,J., Kimura,E., McElhinny,A.S., Pelin,K.,
Witt,C.C., Bang,M.L., Trombitas,K., Granzier,H., Gregorio
Sorimachi,H. and Labeit,S.
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Homo sapiens mRNA for RNF28 gene for ring finger protein 28-
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/db_xref="taxon:9606"
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                                                     GlnAlaValIleThrGlnMetGluGluValCysGlnThrIleGluAspAsnSerArgArg
                                                                                                  GACAAAAAGACTGAACTGAATAACTGTATCTCCATGCTGGTGGCGGGAATGACCGTGTG
                                                                                                                                                                                                                                            HisGluAspGluLysIleAsnIleTyrCysLeuSerCysGluValProThrCysSerLeu 148
                                                                                                                                                                                                                                                                                                               GlnGlu---SerSerArgProLeuHisAlaLysAlaGluGlnHisLeuMetCysGluGlu
                                   CAGACCATCATCACTCAGCTGGAGGATTCCCGTCGAGTGACCAAGGAGAACAGTCACCAG 1047
                                                                                                                                 ArgGlnLysSerGluLeuSerAspGlyIleAlaMetLeuValAlaGlyAsnAspArgVal 188
                                                                                                                                                                TGCAAGGTGTTTGGGATCCACAAGGCCTGCGAGGTGGCCCCATTGCAGAGTGTCTTCCAG
                                                                                                                                                                                             CysLysValPheGlyAlaHisLysAspCysGluValAlaProLeuProThrIleTyrLys 168
                                                                                                                                                                                                                               CACGAAGATGAGAAAATCAACATCTACTGTCTCACGTGTGAGGTGCCCACCTGCTCCATG
                                                                                                                                                                                                                                                                                              CAGGAGTGCTCCAGTCGGCCGCTG-----CAGAAGGGCAGTCACCCCATGTGCAAGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                          TCCATGTCTGGAGGCCGTTTCCGCTGCCCCACCTGCCGCCACGAGGTGATCATGGATCGT
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TQEQEEKLSFIEALIQQYQEQLDKSTKLVETAIQSLDEPGGATFLLTAKQLIKSIVEA
SKGCQLGKTEQGFENMDFFTLDLEHIADALRAIDFGTDEEEEEFIEEEDQEEEESTEG
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475. .1497
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/evidence=not_experimental
475. .1497
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/protein_id="CAC33173.1"
/db_xref="GI:13171051"
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RESULT 16
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                                                                                                                                                                                                                                                                                                                                                                                       Submitted (20-MAR-2000) Stanchi F., (Universita di Padova, Via G. Colombo
                                                                                                                                                                                                                                                                                                                                                                                                                           Stanchi, F.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Characterisation of MURF2, a new muscle-specific RING finger protein of the RBCC family that associates with microtubules
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stanchi, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/Godon_start=1
/product="muscle specific RING
/protein id="CAC81706.1"
/db_xref="GI:18073356"
                                                                                                                                                                                                                        /tissue_type="skeletal
/clone_lib="pEAK8"
                                                                                                                                                                                                                                                            /clone="STRAIT03036"
                                                                                                                                                                                                                                                                                /map="p35.1-35.2"
                                                                                                                                                                                                                                                                                                                /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                        /gene="MURF2"
                                                                                                               /number=
                                                                                                                              /gene="MURF2"
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                                                                                                                                                                                                                                                                                               /chromosome="1"
                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
                                                                                                                                                                                                     dev_stage="adult"
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/translation="mdykssliqdgnpmenlekqlicpiclemftkpvvilpcqhnlc rkCandifqaanpywtsrgssvsmsggrfrcptcrhevimdrhgvyglqrnllvenii

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BASE COUNT
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HisGluAspGluLysIleAsnIleTyrCysLeuSerCysGluValProThrCysSerLeu
                                CAGGAGTGCTCCAGTCGGCCGCTG-----CAGAAGGGCAGTCACCCCATGTGCAAGGAG
                                              GlnGlu---SerSerArgProLeuHisAlaLysAlaGluGlnHisLeuMetCysGluGlu
                                                                                         HisGlyValTyrGlyLeuGlnArgAsnLeuLeuValGluAsnIleIleAspIleTyrLys
                                                                                                                                                                    ValSerSerGlyGlyArgPheArgCysProSerCysArgHisGluValValLeuAspArg
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SVFQGQKTELNNCISMLVAGNDRVQTIITQLEDSRRVTKENSKQVKEELSQKFDTLYA
ILDEKKSELLQRITOEQEKKLISFIEBALIQVYDEQLDKSTKENSKUVETALQSLDEFGGATFL
LTAKQLIKSIVEASKGCQLGKTEQGFENMDFFTLDLEHIADALRAIDFGTDEEEEEFI
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/number=5
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                             Sequence 192
AX274927
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                                                                                                                        Transcription factors
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andman,O., Tang,Y.T.,
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GlnProGlyAlaAlaGlyAspGluGl GlyGluGluGlyAsnAlaGlyLeuGl	Alignment Pred. No.: Score:	BASE COUNT ORIGIN			CDS		FEATURES Sourc		COMMENT	AUTHORS TITLE JOURNAL	TITLE JOURNAL		ind		ACCESSION VERSION KEYWORDS SOURCE	AK056942 LOCUS DEFINITION	5 5	345	10	

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J01) Takao Isogai, Helix Research Institute, 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan L.co.jp, Tel:81-438-52-3975, Fax:81-38-52-3986) lencing project supported by Ministry of Industry of Japan; cDNA full insert sequencing: for Biotechnology (RAB); cDNA library Research Institute (HRI) (supported by Japan pretc.); 5'- & 3'-end one pass sequencing: RAB, 1999 Center, National Institute of Technology and plection for full insert sequencing: RAB and
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s RING-finger protein MURF mRNA.
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KEEGHQ"
517 g
                                                                                KGSHPMCKEHEDEKINIYCLTCEVPTCSMCKVFGIHKACEVAPLQ
ISMLVAGNDRVQTIITQLEDSRRVTKENSHQVKEELSQKFDTLYA
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                                        ATGGACTTCTTTACTTTGGATTTAGAGCACATAGCAGACGCCCTGAGAGCCATTGACTTT
                                                              MetGluGlnPheSerValSerValGluHisValAlaGluMetLeuArgThrIleAspPhe
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                                                                             TGTGCCAATGACATCTTCCAGGCTGCAAATCCCTACTGGACCAGCCGGGGCAGCTCAGTG
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Direct Submission
Submitted (27-FEB-2001) MSF,
USA
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/db_xref="taxon:9606"
/chromosome="1"
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Catarrhini; Hominidae;
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HisGluAspGluLysIleAsnIleTyrCysLeuSerCysGluValProThrCysSerLeu 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         GlyGluGluGlyAsnAlaGlyLeuGluGlu 354
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     Osada, N.,
                                                    Cercopithecinae;
                                                                            Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                              Macaca fascicularis
                                                                                                                                                Macaca fascicularis adult male brain parietal lobe cDNA to mRNA, clone_lib.macaque brain cDNA library QnpA clone:QnpA-10466.
                                                                                                                                                                        fis (full insert sequence).
Macaca fascicularis adult male brain
                                                                                                                                                                                                                               AB047601.1 GI:9929936
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     Hida, M.,
                                                         Macaca.
     Kusuda, J.,
                                                                            Craniata; Vertebrata;
Catarrhini; Cercopith
     Tanuma, R.,
                                                                                                                                                                                                                                                                                 clone:QnpA-10466.
                                                                                                                                                                                                                                                                                                           mRNA
     Iseki, K.,
                                                                            Cercopithecidae;
                                                                                                                                                                                                                                                                                                         linear
                                                                                                      Euteleostomi;
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AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
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       61
                                                                                                                                                                                                                                                                                                         1 MetAsnPheThrValGlyPheLysProLeuLeuGlyAspAlaHisAsnMetAspAsnLeu
                                                                                                                                                        GluLysGlnLeuIleCysProIleCysLeuGluMetPheSerLysProValValIleLeu
                                                                                                                                                                                                                                                         ATGAGCGCATCTCTGAATTACAAGTCTTTTTCCAAAGAGCAGCAGCCATGGATAACTTA
     LeuTrpGlnSerArgGlySerThrThrValSerSerGlyGlyArgPheArgCysProSer
                                                         CCCTGTCAGCACCACCTGTGTAGGAAATGTGCCAGTGATATTTTCCAGGCCTCTAACCCG
                                                                                 ProCysGlnHisAsnLeuCysArgLysCysAlaAsnAspValPheGlnAlaSerAsnPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [ATGTGGCCTTTTTTTTTTTTTTT]; double-stranded cDNA was Synthesized using specific 5' and 3' primers and amplified by PCR. The PCR product was digested with Sfil and size selection was performed to exclude fragments <1.5kb.The Sfil-digested PCR product was cloned into distinct DraIII sites of pME185-FL3. XhoI sites just outside the DraIII sites on be used to isolate the cDNA insert. Libraries were constructed by Sugano et al.(University of Tokyo, Institute of Medical Science). Custom primer used for sequencing [CTCTGGCTCTAAAAGCTGCG];
3' end primer [CGACCTGCAGCTCTAAAAGCTGCG];
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (32-AUG-2000) Katsuyuki Hashimoto, National Institute of Infectious Diseases, Division of Genetic Resources; 23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan (E-mail:khashi@nih.go.jp, URL:http://www.nih.go.jp/yoken/genebank/, Tel:81-3-5285-1111(ex.2120), Fax:81-3-5285-1181)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Suto,Y., Hirai,M., Terao,K., Suzuki,Y., Sugano,S. and Hashimoto,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lab host:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hashimoto, K., Osada, N., Hida, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21458551
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vector:
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a 396 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="msaslnyksfskeQQTmDnLekQLICPICLemfTkPvVILPCQH
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NIIDIYKQESIRPEKKSDQPMCEEHEEERINIYCLNCEVPTCSLCKVFGAHKDCQVAP
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/protein_id="BAB12125.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /dev_stage="adult"
567. .1244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LTHVFQRQKSELSDGIAILVGSNDRVQGVISQLEDTCKTIEECCRKQKQELCEKFDYL
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/clone_lib="macaque brain cDNA library QnpA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Macaca fascicularis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="QnpA-10466"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:9541"
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866.00
77.25%
65.10%
45.29%
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DraIII (CACCATGTG)
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Conservative:
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REFERENCE AUTHORS ACCESSION VERSION

KEYWORDS

ORGANISM

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                                  1212 ----
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                                                                                                                                                                 241 GluLysLeuGlnArgValArgGlyLeuIleArgGlnTyrGlyAsp 255
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Search completed: December 3, 2002, 15:33:45 Job time: 2752 secs

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BB140247 RIKEN full-length enriched, adult male bone Mus musculus
 DEFINITION
             cDNA clone 9830168H24 37, mRNA sequence.
 ACCESS ION
             BB140247
 VERSION
             BB140247.1 GI:8795184
 KEYWORDS
             EST.
 SOURCE
             house mouse.
   ORGANISM
             Mus musculus
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE
                (bases 1 to 316)
             Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci
   AUTHOIS
             ,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N.,
             Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M.,
             Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N.
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             , Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toya
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             , Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
             RIKEN Mouse ESTs (Konno, H., et al.)
   TITLE
   JOURNAL
             Unpublished (2000)
             Contact: Yoshihide Hayashizaki
 COMMENT
             Laboratory for Genome Exploration Research Group, RIKEN Genomic
             Sciences Center(GSC), Yokohama Institute
             The Institute of Physical and Chemical Research (RIKEN)
             1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
             Tel: 81-45-503-9222
             Fax: 81-45-503-9216
             Email: genome-res@gsc.riken.go.jp,
             URL:http://genome.gsc.riken.go.jp/
FEATURES
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                     Project of Genome Exploration Research Group in Riken
                     Genomic Sciences Center and Genome Science Laboratory in
                     RIKEN. Division of Experimental Animal Research in Riken
                     contributed to prepare mouse tissues. 1st strand cDNA was
                     primed with a primer [5'
                     prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by
                     cap-trapper. cDNA went through one round of normalization
                     to Rot = 10.0 and subtraction to Rot = 185.0. Second
                     strand cDNA was prepared with the primer adapter of
                     3']. cDNA was cleaved with XhoI and BamHI. Vector: a
                     modified pBluescript KS(+) after bulk excision from Lambda
                     FLC I."
BASE COUNT
                          91 c
                 67 a
                                  105 q
                                            53 t
ORIGIN
                           7.5%;
                                 Score 108; DB 10; Length 316;
  Best Local Similarity
                          99.4%;
                                 Pred. No. 1.3e-40;
  Matches 158; Conservative
                                 0; Mismatches
                                                   1;
                                                      Indels
                                                                 0; Gaps
                                                                             0:
Qy
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Qy
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Db

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